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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:35:24 ; Search time 4754.26 Seconds
(without alignments)
10548.684 Million cell updates/sec

Title: US-10-623-472-31
Perfect score: 1035
Sequence: 1 atggccaattacacgtgcg.....accattccacgaagtgtaa 1035

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hlg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ete.*
- 12: gb_ey.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	100.0	1035	6	AX521743 Sequence
2	1035	100.0	1546	9	AF015524 Homo sapi
3	1035	100.0	1547	6	AR526903 Sequence
4	1035	100.0	1790	9	AF015525 Homo sapi
5	1031.8	99.7	1475	6	AX454430 Sequence
6	1031.8	99.7	1475	6	AX490908 Sequence
7	1031.8	99.7	1644	6	CQ714577 Sequence
8	1031.8	99.7	1645	6	CQ882060 Sequence
9	1031.8	99.7	1645	6	AX549068 Sequence
10	1031.8	99.7	1698	9	AF014958 Homo sapi
11	1031.8	99.7	1755	9	BC071682 Homo sapi
12	1031.8	99.7	1770	9	BC025717 Homo sapi
13	1031.8	99.7	143068	6	AX335952 Sequence
14	1031.8	99.7	143068	9	HSU95626 Homo sapien
15	1031.8	99.7	185437	9	AC098613 Homo sapi
16	1030.2	99.5	1035	9	AV337001 Homo sapi
17	1030.2	99.5	1645	9	HSU97123 Homo sapien
18	1029.8	99.5	1270	6	AR270193 Sequence
19	1028.6	99.4	1035	9	HS344142 Homo sapi

20	973.4	94.0	1050	6	AR168095	AR168095	Sequence
21	950.2	91.8	1035	9	AF124381	AF124381	Macaca mu
c	695.8	67.2	7644	6	AX345787	AX345787	Sequence
23	651	62.9	7644	6	AX345786	AX345786	Sequence
24	631	61.0	1195	4	AB119274	AB119274	Sus scrof
25	631	61.0	1314	4	AB119273	AB119273	Sus scrof
26	631	61.0	14233	4	AP006435	AP006435	Sus scrof
27	631	61.0	165558	4	AP006185	AP006185	Sus scrof
c	505.2	48.8	588	6	AX079344	AX079344	Sequence
28	443.2	42.8	231984	2	AC112401	AC112401	Rattus no
30	414	40.0	1790	10	AF316576	AF316576	Mus muscu
31	414	40.0	2045	6	AX454145	AX454145	Sequence
32	414	40.0	2045	10	AF030185	AF030185	Mus muscu
33	414	40.0	169165	10	AC118727	AC118727	Mus muscu
34	414	40.0	230772	10	AC132832	AC132832	Mus muscu
35	412.4	39.8	1083	6	AX521744	AX521744	Sequence
36	412.4	39.8	1182	10	MMU318863	AJ318863	Mus muscu
37	412.4	39.8	1793	10	BC038631	BC038631	Mus muscu
38	412.4	39.8	1858	10	AB009384	AB009384	Mus muscu
39	326.4	31.5	620	6	AR379763	AR379763	Sequence
40	259.2	25.0	813	11	BV166071	BV166071	CCRL2_302
41	237.8	23.0	1019	9	AF162000	AF162000	Colobus g
42	237.8	23.0	1019	9	AF162002	AF162002	Colobus g
43	237.8	23.0	1019	9	AF162003	AF162003	Colobus g
44	237.8	23.0	1019	9	AF162004	AF162004	Colobus g
45	237.8	23.0	1019	9	AF162005	AF162005	Colobus g

ALIGNMENTS

RESULT 1	AX521743	Sequence 31 from Patent WO02057779.	1035 bp	DNA	linear	PAT 05-OCT-2002
LOCUS	AX521743					
DEFINITION	Sequence 31 from Patent WO02057779.					
ACCESSION	AX521743					
VERSION	AX521743.1	GI:23572791				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	Boddeke, E.H. and Biber, K.				
AUTHORS						
TITLE	Cloning and expression of a new mcp receptor in glial cells					
JOURNAL	Patent: WO 02057779-A 31 25-JUL-2002;					
	Rijksuniversiteit Groningen (NL)					
FEATURES	Location/Qualifiers					
source	1. .1035					
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	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
misc_feature	1..1035					
	/note="hCCR12 chemokine receptor sequence"					

ORIGIN						
Query Match	100.0%;	Score 1035;	DB 6;	Length 1035;		
Best Local Similarity	100.0%;	Pred. No. 2.8e-284;				
Matches 1035;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	ATGCCCAATTACCGCTGGCACCAGGAGTGAATATATGTCCTCATAGAGGTGAAGTCTG 60				
Db	1	ATGCCCAATTACCGCTGGCACCAGGAGTGAATATGTCCTCATAGAGGTGAAGTCTG 60				
Qy	61	GAGCGGATGAGCAGCAGCAATGTGACAGTATGACGCCCGCAGGCACCTCTGAGCCACGTG 120				
Db	61	GAGCGGATGAGCAGCAGCAATGTGACAGTATGACGCCCGCAGGCACCTCTGAGCCACGTG 120				
Qy	121	GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180				
Db	121	GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180				
Qy	181	CTTATCTCTGTTAAATATATAAAGGACTCAAAAGCGGTGGAATAATCTATCTCTTAAACTTG 240				

181	Db		CTTATCCTGGTAAATAATAAAGGACTCAAA	CGCGTGGAAATAATCTATCTTCTAAACATTG	240
241	Qy		GCAGTTTCTAACTTGTGTCTTGTCTTACCTG	CCCTTCTGGGCTCATGCTGGGGCGAT	300
241	Db		GCAGTTTCTAACTTGTGTCTTGTCTTACCTG	CCCTTCTGGGCTCATGCTGGGGCGAT	300
301	Qy		CCCATGTGTAAATTTCTCATTTGGACTGTAT	TCGTGGGCCCTGTACAGTGAGACATTTTTC	360
301	Db		CCCATGTGTAAATTTCTCATTTGGACTGTAT	TCGTGGGCCCTGTACAGTGAGACATTTTTC	360
361	Qy		AAATTGCCCTTCTGACTGTGCAAGGTACTAG	TGTTTTTGGCAAGGGCAACTTTTTCCTCA	420
361	Db		AAATTGCCCTTCTGACTGTGCAAGGTACTAG	TGTTTTTGGCAAGGGCAACTTTTTCCTCA	420
421	Qy		GCCAGGAGGAGGGGCCCTGTGGGACATCAT	TACAAAGTGTCTGGGATGGGTAAACGCCATT	480
421	Db		GCCAGGAGGAGGGGCCCTGTGGGACATCAT	TACAAAGTGTCTGGGATGGGTAAACGCCATT	480
481	Qy		CTGGCCACTTTTGCCTGTAAATTCGTGGT	TATATAAAGTGTGAGTGTGATGAGTGTGAT	540
481	Db		CTGGCCACTTTTGCCTGTAAATTCGTGGT	TATATAAAGTGTGAGTGTGATGAGTGTGAT	540
541	Qy		TGTCGATTATGACAGAACTCCCTTCTGCG	AGCTGATGAGACATTTCTGGAAGCATTTTCTG	600
541	Db		TGTCGATTATGACAGAACTCCCTTCTGCG	AGCTGATGAGACATTTCTGGAAGCATTTTCTG	600
601	Qy		ACTTTAAAAATGAACAATTTCCGTTCTTG	TCTCCTCCCTTATTTATTTTACATTTTCTCTAT	660
601	Db		ACTTTAAAAATGAACAATTTCCGTTCTTG	TCTCCTCCCTTATTTATTTTACATTTTCTCTAT	660
661	Qy		GTGCAATGTAGAAAAACAATAAGGTTTCA	GAGGAGAGGATATAGCTTTTCAAGCTTGTT	720
661	Db		GTGCAATGTAGAAAAACAATAAGGTTTCA	GAGGAGAGGATATAGCTTTTCAAGCTTGTT	720
721	Qy		TTTGGCGTAAATGTAGTCTTCTGATGTGG	GGCCCTACAATATTTGCAATTTTCTCCTG	780
721	Db		TTTGGCGTAAATGTAGTCTTCTGATGTGG	GGCCCTACAATATTTGCAATTTTCTCCTG	780
781	Qy		TCCACTTTCAAAGAACATTTCTCCCTGAG	TGACTGCAAGAGAGCTACAACTCGGACAAA	840
781	Db		TCCACTTTCAAAGAACATTTCTCCCTGAG	TGACTGCAAGAGAGCTACAACTCGGACAAA	840
841	Qy		AGTGTTTCATCATCAATAACTCATGCGCA	CCCAAGTGTGATCAAGCTTCTCTGCTGAT	900
841	Db		AGTGTTTCATCATCAATAACTCATGCGCA	CCCAAGTGTGATCAAGCTTCTCTGCTGAT	900
901	Qy		GCGTTTCTTGATGGGACATTTAGGAAAT	TACCTCTGCGCTGTTTCCCATCTCGGTAGTAA	960
901	Db		GCGTTTCTTGATGGGACATTTAGGAAAT	TACCTCTGCGCTGTTTCCCATCTCGGTAGTAA	960
961	Qy		ACCCCACTTCAACCCAGGGGCGAGTTGTG	CAACAGGCAATCGAGGGGAAGAACTGACCAT	1020
961	Db		ACCCCACTTCAACCCAGGGGCGAGTTGTG	CAACAGGCAATCGAGGGGAAGAACTGACCAT	1020
1021	Qy		TCCAACCGAAGTGTA	1035	
1021	Db		TCCAACCGAAGTGTA	1035	

RESULT 2	
AF015524	
LOCUS	1546 bp mRNA linear PRI 07-SEP-1998
DEFINITION	Homo sapiens putative chemokine receptor (CRAN-A) mRNA, complete cds.
ACCESSION	AF015524
VERSION	AF015524.1 GI:3550066
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1546)

Query Match 99.7%; Score 1031.8; DB 6; Length 1475;
Best Local Similarity 99.8%; Pred. No. 2.3e-283;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCCATAGAGGTGAACCTG 60
Db 29 ATGCCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCCATAGAGGTGAACCTG 88
Qy 61 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTG 120
Db 89 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTG 148
Qy 121 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 149 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
Qy 181 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 209 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 268
Qy 241 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
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Qy 301 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 329 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 388
Qy 361 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 389 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
Qy 421 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 449 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508
Qy 481 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 509 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
Qy 541 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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Qy 601 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Qy 661 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Qy 721 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 749 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
Qy 781 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 809 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
Qy 841 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 869 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 928
Qy 901 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 929 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 988
Qy 961 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 989 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1048
Qy 1021 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035

Db 1049 TCCACCGAAGTGTA 1063
|||||
RESULT 6
AX490908
LOCUS AX490908
DEFINITION Sequence 15 from Patent WO0200690.
ACCESSION AX490908
VERSION AX490908.1 GI:22323791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Poni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 15 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1. 1475
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ORIGIN
Query Match 99.7%; Score 1031.8; DB 6; Length 1475;
Best Local Similarity 99.8%; Pred. No. 2.3e-283;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCCATAGAGGTGAACCTG 60
Db 29 ATGCCCAATTACAGCTGGCACCAGAGGATGAATATGATGCTCCATAGAGGTGAACCTG 88
Qy 61 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTG 120
Db 89 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCAGCTG 148
Qy 121 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 149 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
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Db 329 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 388
Qy 361 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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Qy 541 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

Db	569	TGTGCAATTTAGCAGAACTCCCTTCCCTGCCAGCTGATGAGACATTCCTGGAAGCATTTTCTG	628
Qy	601	ACTTTAAAAATGAACATTTCCGGTTCTTGCTCCTCCCTCTATTATTTTACATTTCTCTAT	660
Db	629	ACTTTAAAAATGAACATTTCCGGTTCTTGCTCCTCCCTCTATTATTTTACATTTCTCTAT	688
Qy	661	GTGCAAAATGAGAAAAACACTAAAGTTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTTGTT	720
Db	689	GTGCAAAATGAGAAAAACACTAAAGTTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTTGTT	748
Qy	721	TTTGCCGTAATGGTAGTCTTCTTCTGATGTGGGGCCCTACAAATATGCAATTTTTCCTG	780
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Qy	781	TCCACTTTTCAAAGAACACTTCTCCCTGAGTCACTGCAAGAGCAGCTACAAATCTGGACAAA	840
Db	809	TCCACTTTTCAAAGAACACTTCTCCCTGAGTCACTGCAAGAGCAGCTACAAATCTGGACAAA	868
Qy	841	AGTGTTCACATCACTAAACTCATCGCCACCACTGCTGTCATCAACCTCTCCTCTGAT	900
Db	869	AGTGTTCACATCACTAAACTCATCGCCACCACTGCTGTCATCAACCTCTCCTCTGAT	928
Qy	901	GCCTTTCTTGATGGGACATTTAGCAATACTCTGCGCTGTTTCCATCTGCGTAGTAAC	960
Db	929	GCCTTTCTTGATGGGACATTTAGCAATACTCTGCGCTGTTTCCATCTGCGTAGTAAC	988
Qy	961	ACCCCACTTCAACCGAGGGGAGTCTGCAAGGCACATCGAGGGGAAGAACTTGACCAT	1020
Db	989	ACCCCACTTCAACCGAGGGGAGTCTGCAAGGCACATCGAGGGGAAGAACTTGACCAT	1048
Qy	1021	TCCACCGAAGTGTA 1035	
Db	1049	TCCACCGAAGTGTA 1063	
RESULT 7			
LOCUS	CQ714577	1644 bp	DNA linear PAT 03-FEB-2004
DEFINITION	Sequence 511 from Patent WO02068579.		
ACCESSION	CQ714577		
VERSION	CQ714577.1 GI:42275434		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.		
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof		
JOURNAL	Patent: WO 02068579-A 511 06-SEP-2002;		
FEATURES	PE Corporation (NY) (US)		
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Query Match	99.78;	Score 1031.8;	DB 6; Length 1644;
Best Local Similarity	99.84;	Pred. No. 2.3e-283;	
Matches 1033;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	1	ATGCCCAATTTACACGCTGGCACCAAGAGATGAATATGATGTCCTCATAGAGGTGAAC	60
Db	202	ATGCCCAATTTACACGCTGGCACCAAGAGATGAATATGATGTCCTCATAGAGGTGAAC	261
Qy	61	GAGAGCGATGAGGAGAGCAATGTGCAAGATGAGCCCGAGGACCTCTCAGCCCGAGCTG	120
Db	262	GAGAGCGATGAGGAGAGCAATGTGCAAGATGAGCCCGAGGACCTCTCAGCCCGAGCTG	321
Qy	121	GTGCCATCACTCTGCTGCTGTTTGTGATCGGTGCTCTGGACAACTCTCCTGTTGTG	180

Db	322	GTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTCTGGACAACTCTCCTGGTTGTG	381
Qy	181	CTTATCTCTGGTAAATATATAAGAGCTCAAAACGGTGGAAAAATATCTATCTTTAAACCTTG	240
Db	382	CTTATCTCTGGTAAATATATAAGAGCTCAAAACGGTGGAAAAATATCTATCTTTAAACCTTG	441
Qy	241	GCAGTTTCTAACTTGTGTTTCTTGCTTACCTCTGCCCTTCTGGGCTCATGCTGGGGGGAT	300
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Db	502	CCCATGTGTAAAAATCTCATTTGGACTGTACTTCTGCTGGGCTGTACAGTGAACATTTTTC	561
Qy	361	AATGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGGACAAGGGCAACTTTTCTCA	420
Db	562	AATGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGGACAAGGGCAACTTTTCTCA	621
Qy	421	GCAGAGGAGGGTGCCTGTGGCATCATTAAGTGTCTTGGCATGGGTAAACAGCATT	480
Db	622	GCAGAGGAGGGTGCCTGTGGCATCATTAAGTGTCTTGGCATGGGTAAACAGCATT	681
Qy	481	CTGGCCACTTTGCTGAAATTCGTGGTTTATAAACTTCAGATGGAAGACAGAAATACAAG	540
Db	682	CTGGCCACTTTGCTGAAATTCGTGGTTTATAAACTTCAGATGGAAGACAGAAATACAAG	741
Qy	541	TGTGCATTTAGCAGAACTCCCTCTCGCAGCTGATGAGACATTTCTGGAAGCATTTTCTG	600
Db	742	TGTGCATTTAGCAGAACTCCCTCTCGCAGCTGATGAGACATTTCTGGAAGCATTTTCTG	801
Qy	601	ACTTTAAAAATGAACATTTCCGTTCTGCTCCCTCCCTATTTATTTTACATTTCTCTAT	660
Db	802	ACTTTAAAAATGAACATTTCCGTTCTGCTCCCTCCCTATTTATTTTACATTTCTCTAT	861
Qy	661	GTGCAATGAGAAAAACACTAAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT	720
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Qy	841	AGTGTTCACATCACTAAACTCATTCGCCACCACTGCTGTCATCAACCTCTCCTGTAT	900
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Qy	901	GGTGTTCCTGATGGAGCATTTAGCAAAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC	960
Db	1102	GGTGTTCCTGATGGAGCATTTAGCAAAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC	1161
Qy	961	ACCCCACTTCAACCGAGGGGAGTGTGCAAGAGGACATCGAGGGAAGAACTTGACCAT	1020
Db	1162	ACCCCACTTCAACCGAGGGGAGTGTGCAAGAGGACATCGAGGGAAGAACTTGACCAT	1221
Qy	1021	TCCACCGAAGTGTA 1035	
Db	1222	TCCACCGAAGTGTA 1236	
RESULT 8			
LOCUS	CQ882060	1645 bp	DNA linear PAT 11-OCT-2004
DEFINITION	Sequence 1 from Patent WO2004083232.		
ACCESSION	CQ882060		
VERSION	CQ882060.1 GI:54034770		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: WO 2004083232-A 1 30-SEP-2004;

Oxigen Limited (GB)

FEATURES

source

1. .1645

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

203. .1237

/note="unnamed protein product"

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ACCESSION AX549068
VERSION AX549068.1 GI:25813844
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AUTHORS
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JOURNAL
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DEFINITION Homo sapiens chemokine receptor X (CKRX) mRNA, complete cds.
ACCESSION AF014958
VERSION AF014958.1 GI:2305263
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 1698)
AUTHORS Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.
TITLE Haplotype analysis of a gene cluster containing CCR5 and a new
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

member of chemokine receptor gene family
Unpublished
2 (bases 1 to 1698)
Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.
Direct Submission
Submitted (18-JUL-1997) Molecular and Human Genetics, Baylor
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LOCUS

DEFINITION

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clone MGC:34104 IMAGE:5228561), complete cds.

ACCESSION

BC025717

VERSION

BC025717.1

KEYWORDS

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SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1770)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

JOURNAL

Strausberg, R.

PUBMED

Direct Submission

AUTHORS

Submitted (06-MAR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>Contact: nisc.mgc@nih.gov

Akher, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

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Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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RESULT 14

HSU95626

LOCUS

DEFINITION Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6

143068 bp DNA linear PRI 16-MAY-1997

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ACCESSION U95626
VERSION U95626.1
KEYWORDS GI:2104517
SOURCE HTG.
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 143068)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
2 (bases 1 to 143068)
AUTHORS McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D.,
Nhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K.,
Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,
Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M.,
Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E.,
Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y.,
Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.
Human BAC clone 110P12
Unpublished (1997)
2 (bases 1 to 143068)
AUTHORS McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D.,
Nhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutz, K.,
Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,
Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M.,
Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E.,
Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y.,
Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.
Direct Submission
TITLE Submitted (27-MAR-1997) Advanced Genome Sequence Analysis Course,
JOURNAL Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor,
NY 11724, USA
COMMENT Regions with single-strand coverage are as follows:
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Query Match 99.7%; Score 1031.8; DB 9; Length 143068;
Best Local Similarity 99.8%; Pred. No. 2.8e-283;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 15
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LOCUS Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.
DEFINITION AC098613 185437 bp DNA linear PRI 01-AUG-2002
AC098613
AC098613
VERSION AC098613.2 GI:22038607
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Unpublished
2 (bases 1 to 185437)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
Submitted (26-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 185437)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Submitted (01-AUG-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Aug 1, 2002 this sequence version replaced gi:16445164.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwgctg@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP11-24F11 (bc0137)
----- Summary Statistics
Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET; 93% of reads
Chemistry: Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 184860 bases at least Q40
Consensus quality: 185398 bases at least Q30
Consensus quality: 185435 bases at least Q20
Insert size: 185437; sum-of-contigs
Quality coverage: 7.6x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': BAC-110P12 U95626, 111014-bp overlap
3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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AUTHORS	1 (bases 1 to 1793) Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zerbahn, H., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, B., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Spaplen, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toohy, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E., Schnarch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (36), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1793) Strausberg R.
AUTHORS	Direct Submission
TITLE	Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapsb-rc@mail.nih.gov Tissue Procurement: Marcello Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: anadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 83 Row: b Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8567367. Location/Qualifiers 1..1793 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="MGC:47919 IMAGE:1347006" /tissue_type="Mammary gland" /clone_lib="Soares_mammary_gland_NbMWG" /lab_host="DH10B" /notes="Vector: pT7T3-Pac" 1..1793 /gene="Ccr12" /notes="synonyms: L-CCR, E01, CCR11" /db_xref="LocusID:54199" /db_xref="MGI:1920904" 178..1260 /gene="Ccr12" /codon_start=1 /product="Ccr12 protein" /protein_id="AAH38631.1" /db_xref="GI:24047249"
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AB009384.1 GI:3090450
VERSION
L-CCR.
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1 (sites)
Shimada,T., Matsumoto,M., Tatsumi,Y., Kanamaru,A. and Akira,S.
A novel lipopolysaccharide inducible C-C chemokine receptor related
gene in murine macrophages
FEBS Lett. 425 (3), 490-494 (1998)
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MEDLINE
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PUBMED
REFERENCE
2 (bases 1 to 1858)
Akira,S. and Shimada,T.
Direct Submission
Submitted (02-DEC-1997) Shizuoka Akira, Hyogo College of Medicine,
Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo
663-8501, Japan (E-mail:akira@hyo-med.ac.jp, Tel:+81-798-45-6357,
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AUTHORS			Luo, Y., Berman, M.A., Fischer, F.R., Abromson-Leeman, S.R., Kuziel, W.A., Gerard, C. and Dorf, M.E.		
TITLE			RANTES and eotaxin stimulate chemotaxis, chemokine/cytokine synthesis, and receptor modulation in murine astrocytes		
JOURNAL			Unpublished		
REFERENCE			2 (bases 1 to 1790)		
AUTHORS			Berman, M.A. and Dorf, M.E.		
TITLE			Direct Submission		
JOURNAL			Submitted (25-OCT-2000) Pathology, Harvard Medical School, 200 Longwood Ave., Boston, MA 02115, USA		
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Qy 661 ATATCTGCTCGAGCACTGAGGAGGAGGAGCTTCAGGAGAGACATGACGCTC 720
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LOCUS
AC118727
DEFINITION Mus musculus chromosome 9, clone RP24-166N8, complete sequence.
AC118727
ACCESSION
VERSION AC118727.7 GI:50582829

KEYWORDS
SOURCE
ORGANISM

HTG.
Mus musculus (house mouse)
Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 169165)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 9, clone RP24-166N8
Unpublished
2 (bases 1 to 169165)

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,I., Campopiano,L., Chang,J.,
Chazaro,B., Choquet,Y., Collange,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faroo,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gordon,S., Goyette,M., Graham,L., Grand-Pierre,N., Jones,C.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Lander,B., Lechoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mieng,L., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Olivier,J., Peterson,K., Phunkhang,P., Riese,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (20-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 169165)

Birren,B., Nusbaum,C., Lander,E., Abouelkhalil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boquelavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choquet,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
DeArrellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
Erickson,J., Faroo,S., Ferreira,P., FitzGerald,M., Gage,D.,
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
MacLean,C., MacDonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mieng,L., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neill,D., Olivier,J., Peterson,K.,
Phunkhang,P., Riese,C., Rogov,P., Roman,J., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (15-MAY-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 169165)

Birren,B., Nusbaum,C., Lander,E., Abouelkhalil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boquelavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choquet,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
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Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, B., Oliver, J., Peterson, K., PhunKhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (24-JUL-2004) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 24, 2004 this sequence version replaced gi:47270724.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@broad.mit.edu

----- Project Information

Center project name: L25144

Center Clone name: 166_N_8

FEATURES

source

Location/Qualifiers

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Matches 1082; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION	Mus musculus chromosome 9, clone RP23-48D19, complete sequence.		
ACCESSION	AC132832		
VERSION	AC132832.13	GI:50540835	
KEYWORDS	HTG.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	(bases 1 to 230772)	
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.		
TITLE	Mus musculus chromosome 9, clone RP23-48D19		

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 230772)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL
REFERENCE
AUTHORS

3 (bases 1 to 230772)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafes, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

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JOURNAL
REFERENCE
AUTHORS

4 (bases 1 to 230772)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafes, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (23-JUL-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Db	210399	AGCAGGTGTTTCCAAACATCCTCCTCTGTGCAAGGATACAGGGTGTGTTTCCCAAGGG	210458
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Qy	901	CCGCTGCTCTATTGCTTCTTGACCGGAAGGCTTTATGATACCTTCGAGCCTGCTC	960
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Qy	961	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGCTATCAGCAAGCCCTCCAAAGG	1020
Db	210999	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGCTATCAGCAAGCCCTCCAAAGG	211058
Qy	1021	GAAGGTCATGCGAGCCCATTTGAATCTGTACAGCAATTTGATCAAGGAGGATATAATA	1080
Db	211059	GAAGGTCATGCGAGCCCATTTGAATCTGTACAGCAATTTGATCAAGGAGGATATAATA	211118
Qy	1081	TAA 1083	
Db	211119	TAA 211121	
RESULT 7			
LOCUS	MMU318863	1182 bp	mRNA linear ROD 01-OCT-2001
DEFINITION	Mus musculus mRNA for putative G-protein coupled beta chemokine receptor (CCR11 gene).		
ACCESSION	AJ318863		
VERSION	AJ318863.1	GI:15886862	
KEYWORDS	CCR11 gene; G-protein coupled beta chemokine receptor.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1		
AUTHORS	Biber, K.P.H.		
TITLE	Cloning and characterisation of a new MCP-1 chemokine receptor		
JOURNAL	CCR11 Unpublished		
REFERENCE	2		
AUTHORS	Zuurman, M.W.		
TITLE	LPS induced expression of a novel MCP chemokine receptor (CCR11) in mouse glial cells in vitro and in vivo		
JOURNAL	Unpublished		

REFERENCE	3 (bases 1 to 1182)		
AUTHORS	Biber, K.P.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-AUG-2001) Biber, K.P.H., Medical Physiology, State University Groningen, Ant. Deusinglaan 1, 9713 AV Groningen, NETHERLANDS		
FEATURES	Location/Qualifiers		
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ORIGIN	Query Match 99.4%; Score 1076.6; DB 10; Length 1182; Best Local Similarity 99.6%; Pred. No. 2.2e-258; Indels 0; Gaps 0; Matches 1079; Conservative 0; Mismatches 0;		
Qy	1	ATGGATAACTACACAGTGGCCCCCGACGATGAATATGATGTCTTAATCTTAGACGACTAC	60
Db	59	ATGGATAACTACACAGTGGCCCCCGACGATGAATATGATGTCTTAATCTTAGACGACTAC	118
Qy	61	CTGGAACAACAGTGGCGGACCAAGTTCCGGCCCCCGAGTTCTCTCCCCCAGCAGGTG	120
Db	119	CTGGAACAACAGTGGCGGACCAAGTTCCGGCCCCCGAGTTCTCTCCCCCAGCAGGTG	178
Qy	121	CTGCAGTCTCTGCTGCGGCTGTTTGGCGTGGTCTCTTGGACACGCTCTCGCGGTGTTT	180
Db	179	CTGCAGTCTCTGCTGCGGCTGTTTGGCGTGGTCTCTTGGACACGCTCTCGCGGTGTTT	238
Qy	181	ATCTTGGTGAATACAAAGGACCAAGATCTGGGGAACATCTACTTCTTAAACCTGGCA	240
Db	239	ATCTTGGTGAATACAAAGGACCTCAGAACTCTGGGGAACATCTACTTCTTAAACCTGGCA	298
Qy	241	CTTTCAAACCTGTGTTCTCTGTTCCCTCCCTGCGGTTCTGGGCCCATATCTGACGACACGGG	300
Db	299	CTTTCAAACCTGTGTTCTCTGTTCCCTCCCTGCGGTTCTGGGCCCATATCTGACGACACGGG	358
Qy	301	GAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCCGACTCCCACTCTCGGGCTTATAC	360
Db	359	GAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCCGACTCCCACTCTCGGGCTTATAC	418
Qy	361	AGCGAGTGTGTTTCCAAACATCTCTCTCTTGTGTCAAGGATACAGGGTGTGTTTCCCAAGGG	420
Db	419	AGCGAGTGTGTTTCCAAACATCTCTCTCTTGTGTCAAGGATACAGGGTGTGTTTCCCAAGGG	478
Qy	421	CGACTGCGCTCCATCTTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCTCTGCGCATGG	480
Db	479	CGACTGCGCTCCATCTTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCTCTGCGCATGG	538
Qy	481	GCCATGGCTACTGCGCTCTCTTTGGCCCGAGTCTGTGTTTATGAGCCTCGATGGAAGA	540
Db	539	GCCATGGCTACTGCGCTCTCTTTGGCCCGAGTCTGTGTTTATGAGCCTCGATGGAAGA	598

Qy	541	CAGAAACAAAGTGTGCTTTGGCAACCTCACCTTTGCGCAATCGAAGCGCGCTCTGG	600
Db	599	CAGAAACAAAGTGTGCTTTGGCAACCTCACCTTTGCGCAATCGAAGCGCGCTCTGG	658
Qy	601	AAGTACGTTCTGACGTCAGAAATGATCATCTTGGTACTTGGCTTTTCCCTCTGCTGGTTTTT	660
Db	659	AAGTACGTTCTGACGTCAGAAATGATCATCTTGGTACTTGGCTTTTCCCTCTGCTGGTTTTT	718
Qy	661	ATAATCTGCTGACGGCAACTGAGAGAAAGCAGAGCTTTCAGGAGAGACAGATGACACCTC	720
Db	719	ATAATCTGCTGACGGCAACTGAGAGAAAGCAGAGCTTTCAGGAGAGACAGATGACACCTC	778
Qy	721	CACAAGCGGCTCTTGTATACAGGGGCTGCTCTTTTGTATGTGGGCGCTTACACACT	780
Db	779	CACAAGCGGCTCTTGTATACAGGGGCTGCTCTTTTGTATGTGGGCGCTTACACACT	838
Qy	781	GTGCTTTTCCCTGCTGCTTTCCAGGAACACTTGTCCCTGAGGATGAGAGAGCAGCTAC	840
Db	839	GTGCTTTTCCCTGCTGCTTTCCAGGAACACTTGTCCCTGAGGATGAGAGAGCAGCTAC	898
Qy	841	CACCTGACGCAAGTGTTCAGGTACACAGCTGTGTAGCGACCAACCACTGCTGGTCAAC	900
Db	899	CACCTGACGCAAGTGTTCAGGTACACAGCTGTGTAGCGACCAACCACTGCTGGTCAAC	958
Qy	901	CCGCTGCTCTATTGCTTCTTGACCGGAAGCGCTTTATGAGATACCTTCGACGCTGTTTC	960
Db	959	CCGCTGCTCTATTGCTTCTTGACCGGAAGCGCTTTATGAGATACCTTCGACGCTGTTTC	1018
Qy	961	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGGCTATCAGCAAGCGCTTCCAAGG	1020
Db	1019	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGGCTATCAGCAAGCGCTTCCAAGG	1078
Qy	1021	GAAGGTCAATGGAGGCCATTTGAATCTGACAGAAATTTGCATCAAGGCGAGATATAATA	1080
Db	1079	GAAGGTCAATGGAGGCCATTTGAATCTGACAGAAATTTGCATCAAGGCGAGATATAATA	1138
Qy	1081	TAA 1083	
Db	1139	TAA 1141	
RESULT 8			
LOCUS	AX454145	2045 bp	DNA linear PAT 06-JUL-2002
DEFINITION	Sequence 29 from Patent WO0203793.		
ACCESSION	AX454145		
VERSION	AX454145.1	GI:21713776	
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Mus musculus		
REFERENCE	1		
AUTHORS	Allen, K.D. and Brennan, T.J.		
TITLE	Transgenic mice containing targeted gene disruptions		
JOURNAL	Patent: WO 0203793-A 29 17-JAN-2002;		
Delegen, Inc. (US)			
FEATURES	Location/Qualifiers		
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ORIGIN			
Query Match	99.4%	Score 1076.6; DB 6; Length 2045;	
Best Local Similarity	99.6%;	Pred. No. 2.2e-258;	
Matches 1079; Conservative	0; Mismatches 4; Indels 0; Gaps 0;		
Qy	1	ATGATTAATCTACAGTGGCGCCCGGACGATGAATATGATGCTCTTAATCTTAGAGGACTAC	60
Db	445	ATGATTAATCTACAGTGGCGCCCGGACGATGAATATGATGCTCTTAATCTTAGAGGACTAC	504

Qy	61	CTGGCAACAGTGGGCGCGACCAAGTTCCGGCCCGAGTTCTCTCCCGCCAGAGGTG	120
Db	505	CTGGCAACAGTGGGCGCGACCAAGTTCCGGCCCGAGTTCTCTCCCGCCAGAGGTG	564
Qy	121	CTGCAGTCTTCTGCTGCGCGGTGTTTGGGTGGGTCTCTTGGACAAACGTGCTGGCGGTGTTT	180
Db	565	CTGCAGTCTTCTGCTGCGCGGTGTTTGGGTGGGTCTCTTGGACAAACGTGCTGGCGGTGTTT	624
Qy	181	ATCTTGGTGAATACAAAGACTCAAGAATCTGGGGAACATCTACTTCTTAAACCTGGCA	240
Db	625	ATCTTGGTGAATACAAAGACTCAAGAATCTGGGGAACATCTACTTCTTAAACCTGGCA	684
Qy	241	CTTTCAAACCTGTGTTTCTCTGCTTCCCTGCGCGTCTGGGCCCATACTGACAGACACGGG	300
Db	685	CTTTCAAACCTGTGTTTCTCTGCTTCCCTGCGCGTCTGGGCCCATACTGACAGACACGGG	744
Qy	301	GAAGCCCTGGCAACCGGACCTGTAAAGTCTTGTGCGGACTCCACTCTCTCGGGCTTATAC	360
Db	745	GAAGCCCTGGCAACCGGACCTGTAAAGTCTTGTGCGGACTCCACTCTCTCGGGCTTATAC	804
Qy	361	AGCGAGGTGTTTCCCAACATCTCTCTCTGTGCAAGGATACAGGGTGTGTTTCCCAAGGG	420
Db	805	AGCGAGGTGTTTCCCAACATCTCTCTCTGTGCAAGGATACAGGGTGTGTTTCCCAAGGG	864
Qy	421	CGACTGGCCCTCCACTCTTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCTCGGATGG	480
Db	865	CGACTGGCCCTCCACTCTTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCTCGGATGG	924
Qy	481	GCCATGGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTTATGAGCTCGGATGGAAGA	540
Db	925	GCCATGGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTTATGAGCTCGGATGGAAGA	984
Qy	541	CAGAAACAGAGTGTGCTTTCGCAACCTCACTCTTCCCATCGAAGCGCGCTCTGG	600
Db	985	CAGAAACAGAGTGTGCTTTCGCAACCTCACTCTTCCCATCGAAGCGCGCTCTGG	1044
Qy	601	AAGTACGTTCTGACGTCAGAAATGATCATCTTGGTACTTGTCTTTCTCTGCTGGTTTTT	660
Db	1045	AAGTACGTTCTGACGTCAGAAATGATCATCTTGGTACTTGTCTTTCTCTGCTGGTTTTT	1104
Qy	661	ATAATCTGCTGACGCAACTGAGGAGAAAGCAGAGCTTTCAGGAGAGACAGATGACGCTC	720
Db	1105	ATAATCTGCTGACGCAACTGAGGAGAAAGCAGAGCTTTCAGGAGAGACAGATGACGCTC	1164
Qy	721	CACAAGCGGCTCTTCTCATACCGGCGGTGTTCTCTTTTGATGTGGCGCTTACACACT	780
Db	1165	CACAAGCGGCTCTTCTCATACCGGCGGTGTTCTCTTTTGATGTGGCGCTTACACACT	1224
Qy	781	GTGCTTTTCTGCTGCTCTTTCCAGGAACACTTGTCCCTGCGAGATGAGAGAGAGCTAC	840
Db	1225	GTGCTTTTCTGCTGCTCTTTCCAGGAACACTTGTCCCTGCGAGATGAGAGAGAGCTAC	1284
Qy	841	CACCTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACCAACCACTGCTGGTCAAC	900
Db	1285	CACCTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACCAACCACTGCTGGTCAAC	1344
Qy	901	CGGCTGCTCTATTGCTTCTTGACCGGAAGCGCTTTATGAGATACCTTTCGACGCTGTTTC	960
Db	1345	CGGCTGCTCTATTGCTTCTTGACCGGAAGCGCTTTATGAGATACCTTTCGACGCTGTTTC	1404
Qy	961	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGGCTTATCAGCAAGCGCTTCCAAGG	1020
Db	1405	CCAGGTGCAATGATATCCCTATCAAGTAGTGGAGGCTTATCAGCAAGCGCTTCCAAGG	1464
Qy	1021	GAAGGTCAATGGAGGCCATTTGAATCTGATCAGCAATTTGCATCAAGGCGAGGATATAATA	1080
Db	1465	GAAGGTCAATGGAGGCCATTTGAATCTGATCAGCAATTTGCATCAAGGCGAGGATATAATA	1524
Qy	1081	TAA 1083	
Db	1525	TAA 1527	

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RESULT 9
AF030185      2045 bp      mRNA      linear      ROD 18-NOV-1997
LOCUS
DEFINITION    Mus musculus putative beta chemokine receptor (E01) mRNA, complete
               cds.
ACCESSION     AF030185
VERSION       AF030185.1  GI:2623640
KEYWORDS
SOURCE        Mus musculus (house mouse)
ORGANISM
REFERENCE     1 (bases 1 to 2045)
AUTHORS       Berman, M.A. and Dorf, M.E.
TITLE         Mus. musculus E01 mRNA, complete cds
JOURNAL       Unpublished (1997)
REFERENCE     2 (bases 1 to 2045)
AUTHORS       Berman, M.A. and Dorf, M.E.
TITLE         Direct Submission
JOURNAL       Submitted (15-OCT-1997) Pathology, Harvard University Medical
               School, 200 Longwood Avenue, Boston, MA 02115-5701, USA
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             CDS
             99.4%; Score 1076.6; DB 10; Length 2045;
             Best Local Similarity 99.6%; Pred. No. 2.2e-258;
             Matches 1079; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGATAACTACAGTGGCCCGGACGATGATATATGATGTCCTTAATCTTAGACGACTAC 60
DB 445 ATGATAACTACAGTGGCCCGGACGATGATATGATGTCCTTAATCTTAGACGACTAC 504

QY 61 CTGGACAACAGTGGCCCGGACCAAGTTCGGGCCCGCCGAGTTCCTCTCCCGCCGACGAGTG 120
DB 505 CTGGACAACAGTGGCCCGGACCAAGTTCGGGCCCGCCGAGTTCCTCTCCCGCCGACGAGTG 564

QY 121 CTGCAGTTCCTGCTGCGCGGTGTTGGCGGTGCTCTTGGACACGCTGCTGGCGGTGTTT 180
DB 565 CTGCAGTTCCTGCTGCGCGGTGTTGGCGGTGCTCTTGGACACGCTGCTGGCGGTGTTT 624

QY 181 ATCTTGTGTAATACAAAGACATCAAGAATCTGGGGAACATCTACTTCTTAAACCTGGCA 240
DB 625 ATCTTGTGTAATACAAAGACATCAAGAATCTGGGGAACATCTACTTCTTAAACCTGGCA 684

QY 241 CTTTCAAACTGTGTTTCTGCTTCCCTCGCGGTTCGGGCCCACTATCGACGACACGGG 300
DB 685 CTTTCAAACTGTGTTTCTGCTTCCCTCGCGGTTCGGGCCCACTATCGACGACACGGG 744

QY 301 GAAAGCCCTGGCAACGGGACCTGTAAGTCTTGTGCGACTCCCACTCTCGGCTTATAC 360
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ORIGIN

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Query Match      99.4%; Score 1076.6; DB 10; Length 2045;
Best Local Similarity 99.6%; Pred. No. 2.2e-258;
Matches 1079; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGATAACTACAGTGGCCCGGACGATGATATATGATGTCCTTAATCTTAGACGACTAC 60
DB 445 ATGATAACTACAGTGGCCCGGACGATGATATGATGTCCTTAATCTTAGACGACTAC 504

QY 61 CTGGACAACAGTGGCCCGGACCAAGTTCGGGCCCGCCGAGTTCCTCTCCCGCCGACGAGTG 120
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QY 121 CTGCAGTTCCTGCTGCGCGGTGTTGGCGGTGCTCTTGGACACGCTGCTGGCGGTGTTT 180
DB 565 CTGCAGTTCCTGCTGCGCGGTGTTGGCGGTGCTCTTGGACACGCTGCTGGCGGTGTTT 624

QY 181 ATCTTGTGTAATACAAAGACATCAAGAATCTGGGGAACATCTACTTCTTAAACCTGGCA 240
DB 625 ATCTTGTGTAATACAAAGACATCAAGAATCTGGGGAACATCTACTTCTTAAACCTGGCA 684

QY 241 CTTTCAAACTGTGTTTCTGCTTCCCTCGCGGTTCGGGCCCACTATCGACGACACGGG 300
DB 685 CTTTCAAACTGTGTTTCTGCTTCCCTCGCGGTTCGGGCCCACTATCGACGACACGGG 744

QY 301 GAAAGCCCTGGCAACGGGACCTGTAAGTCTTGTGCGACTCCCACTCTCGGCTTATAC 360
DB 745 GAAAGCCCTGGCAACGGGACCTGTAAGTCTTGTGCGACTCCCACTCTCGGCTTATAC 804

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RESULT 10

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AC112401/c
LOCUS
DEFINITION    Rattus norvegicus clone CH230-182H10, *** SEQUENCING IN PROGRESS
               *** 3 unordered pieces.
AC112401
VERSION        AC112401.4  GI:23270069
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
               1 (bases 1 to 231984)
REFERENCE
AUTHORS        Muzny, D., Marle, J., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
               Allen, C., Allen, H., Albrooke, S., Amin, A., Anguiano, D.,
               Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
               Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
               Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
               Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,

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QY 361 AGCGAGGTGTTTCCAACTCCTCTCTGTGTCAAGGATACAGGGTGTGTTTCCCAAGGG 420
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QY 421 CGACTGGCCCTCCATCTTTCAAGACAGTGTCTTGTGGTATTTGTGGTGTGATCTCTGGCATGG 480
DB 865 CGACTGGCCCTCCATCTTTCAAGACAGTGTCTTGTGGTATTTGTGGTGTGATCTCTGGCATGG 924

QY 481 GCCATGGCTACTGGGCTCTCTTTGCCCGAGTCTCTGTGTTTATGAGCCTCGATGGAAGA 540
DB 925 GCCATGGCTACTGGGCTCTCTTTGCCCGAGTCTCTGTGTTTATGAGCCTCGATGGAAGA 984

QY 541 CAGAAACACAAGTGTGCTTTGGCAAACTCCTCTTTCGCAATCGAAGCCCGCTCTGG 600
DB 985 CAGAAACACAAGTGTGCTTTGGCAAACTCCTCTTTCGCAATCGAAGCCCGCTCTGG 1044

QY 601 AAGTACGTTCTGAGCTCAAAAATGATCATCTTGTGACTTGTCTTCTCTCTCTCTCTCTCTCT 660
DB 1045 AAGTACGTTCTGAGCTCAAAAATGATCATCTTGTGACTTGTCTTCTCTCTCTCTCTCTCTCT 1104

QY 661 ATAATCTGCTGCAGGCAACTGAGGAGAGGAGGAGAGCTTCAGGAGAGAGACAGTACGACCTC 720
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QY 721 CACAAGCCGCTCTTTGTCATAACGGGCGTGTCTCTTTGATGTGGGCGCTTACAACACT 780
DB 1165 CACAAGCCGCTCTTTGTCATAACGGGCGTGTCTCTTTGATGTGGGCGCTTACAACACT 1224

QY 781 GTGCTTTTCTGCTGCTTTTCCAGGAACACTTGTCTCTCGAGGATGAGAGAGAGCTAC 840
DB 1225 GTGCTTTTCTGCTGCTTTTCCAGGAACACTTGTCTCTCGAGGATGAGAGAGAGCTAC 1284

QY 841 CACTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACACCACTGCTGGGTCAAC 900
DB 1285 CACTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACACCACTGCTGGGTCAAC 1344

QY 901 CCCTGCTCTATTGCTTCTTGAACCGAAGCCCTTTATGAGATACCTTCGAGGCTGTTC 960
DB 1345 CCCTGCTCTATTGCTTCTTGAACCGAAGCCCTTTATGAGATACCTTCGAGGCTGTTC 1404

QY 961 CCAGGTGCAATGATATCCCTTATCAAGTAGTGAGGCTATCAGCAAGCCCTCCAGG 1020
DB 1405 CCAGGTGCAATGATATCCCTTATCAAGTAGTGAGGCTATCAGCAAGCCCTCCAGG 1464

QY 1021 GAAGGTGATGCGAGGCCATTGAACCTGTACAGCAATTTGATCAAAAGCAGATATATA 1080
DB 1465 GAAGGTGATGCGAGGCCATTGAACCTGTACAGCAATTTGATCAAAAGCAGATATATA 1524

QY 1081 TAA 1083
DB 1525 TAA 1527

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Cardenas, V., Carter, K., Cavazos, J., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flegg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabist, A., Gante, R., Garcia, A., Garner, I., Garza, M., Gubregorge, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, C., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulvik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenuhewa, L., Loulseg, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okunolu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Prannkoch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasaana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Woodden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiser, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished
2 (bases 1 to 231984)

Worley, K.C.

Direct Submission

Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 231984)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 23, 2002 this sequence version replaced gi:21739980.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRU

Center clone name: CH230-182H10

----- Summary Statistics
Assembly program: Phrap; version 0.950329
Consensus quality: 166231 bases at least Q40
Consensus quality: 171002 bases at least Q30
Consensus quality: 174772 bases at least Q20
Estimated insert size: 190923; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 137707: contig of 137707 bp in length
* 137708 137807: gap of unknown length
* 137808 218965: contig of 81158 bp in length
* 218966 219065: gap of unknown length
* 219066 231984: contig of 12919 bp in length.

FEATURES

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DEFINITION Sus scrofa CCRL2 mRNA for chemokine C-C motif receptor-like 2, complete cds, transcript variant B.
ACCESSION AB119274
VERSION AB119274.1 GI:44890883
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
1 Shinkai,H., Morozumi,T., Toki,D., Eguichi,T., Muneta,Y., Awata,T. and Uenishi,H.
Analysis of genomic structure of porcine CC chemokine receptor genes and their expression
Unpublished
2 (bases 1 to 1195)
Shinkai,H. and Uenishi,H.
Direct Submission
Submitted (03-SEP-2003) Hiroki Shinkai, STAFF-Institute, Second Research Division; 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan (E-mail:sinkai@gene.staff.or.jp, Tel:81-29-838-2190, Fax:81-29-838-2337)

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Matches 695; Conservative 0; Mismatches 379; Indels 9; Gaps 3;
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VERSION   AP006435.1 GI:41688301
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ORGANISM Sus scrofa (pig)
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REFERENCE 1
AUTHORS   Shinkai,H., Morozumi,T., Toki,D., Muneta,Y., Awata,T. and
          Unishi,H.
TITLE     Cloning of porcine CC chemokine receptor genes and clustering
          structure on SSC13
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 144233)
AUTHORS   Shinkai,H. and Unishi,H.
TITLE     Direct Submission
JOURNAL   Submitted (12-MAY-2003) Hiroki Shinkai, STAFF-Institute; 446-1
          Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan
          (E-mail:sinkaio@gene.staff.or.jp, Tel:81-29-838-2190,
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ORIGIN

Query Match      39.6%;   Score 428.6;   DB 4;   Length 144233;
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Matches 695;   Conservative 0;   Mismatches 379;   Indels 9;   Gaps 3;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Kits, such as nucleic acid arrays, comprising a majority of
TITLE humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 511 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1.1644
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 39.1%; Score 423.6; DB 6; Length 1644;
Best Local Similarity 65.6%; Pred. No. 5.7e-95;
Matches 710; Conservative 0; Mismatches 339; Indels 33; Gaps 5;
Qy 1 ATGATAACTACACAGTGGCCCGGACGATGATATGATGCTCTTAATCTTTAGACGACTAC 60
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Db 202 ATGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCC---TCATAGAAGGTGAA 258
Qy 61 CTGGCAACACAGTGGGCGCGGACCAAGTT-----CCGGCGCCCGGAGTTCTCTCCCCCAG 114
Db 259 CTGGAGAGCGATGAGGCGAGAGCAATGTGACAAAGTATGACGCCCAGGCACTCTCAGCCAG 318
Qy 115 CAGGTCTCGAGTCTTCTGCTGGCGGTGTTTTCGGGTGGTCTCTTGGACAACAGTGTCTGGCG 174
Db 319 CTGGTGCCTATCATCTCTGCTCTGCTGTGTTGTGTGATCGGTGTCTTGAGCAATCTCCTG 378
Qy 175 GTGTTTATCTTGTGTAATAACAAAGGACTCAAGAACTCGGGAAACATCTACTTCTCTAAAC 234
Db 379 GTGCTTATCTGTGTAATAATAAAGGACTCAAGCGGTGGAATAATCTATCTTCTTAAC 438
Qy 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCGGGCCCACTATCGAGCA 294
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Qy 295 CACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCCTTGTGCGACTCCTCTCTCGGGC 354
Db 494 -----GGGGCGATCCCATGTGTAAAAATTTCTCATTTGGAAGTACTCTTCTGTTGGC 540
Qy 355 TTATACAGCGAGGTGTTTCCAAACATCTCTCTTGTGCAAGCATACAGGGGTGTTTTC 414
Db 541 CTGTACAGTGAACATTTTTCATTTGCCCTCTGACTGTGCAAGGTACTCTAGTGTGTTTG 600
Qy 415 CAAAGCGCAG---TGCGCTCCATCTTTCAGACAGTGTCTTGTGTTGTTGTTGCGTCAATC 471
Db 601 CACAAGGAAACTTTTCTCAGCAGGAGGAGGTGCGCTGTGGCATCATTAAGGTGTC 660
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Db 661 CTGGCATGGGTAAACAGCCATTTGCGCCACTTTGCGCTGAATTCGTGGTTTATAAAGCTCAG 720
Qy 532 ATGGAAGACAGAAAACAAAGTGTGCTTTGGCAAACTCCTCCTTTGCAATCGAAGCG 591
Db 721 ATGGAAGACAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 780
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Qy 892 TCGTCAACCCGCTGCTCTATTTTGTCTTTGACCGGAAGCGCTTTATGAGATACCTTCGC 951
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Qy 952 AGCTGTTTCCACGGTGAATGATATCCCTATCAAAAGTGTGAGGCTATCAGAGCG 1011
Db 1138 CGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAGGC 1197
Qy 1012 CTTCCAAAGGAGGTTCATGTGCGAGGCCCATTTGTAAGTGTGATAGATACCTTCGC 1071
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Qy 1072 GA 1073
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Db 1358 GA 1259

Search completed: June 18, 2005, 09:52:58
Job time : 4979.74 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:38:50 ; Search time 3956.26 Seconds
(without alignments)
9958.019 Million cell updates/sec

Title: US-10-623-472-31

Perfect score: 1035

Sequence: 1 atggccaattacacgtgcg.....accattccaccgaagttaa 1035

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737.8	71.3	896	5	BQ892457
2	677	65.4	716	7	CF147784
3	637.8	61.6	729	6	CD370587
4	617.6	59.7	720	6	CD520843
5	609.8	58.9	831	4	BI834559
6	594.4	57.4	773	7	CO959196
7	526.6	50.9	880	4	BI819787
8	470.2	45.4	750	2	BE871331
9	440.4	42.6	768	6	CD468404
10	433	41.8	1035	4	EG386374
11	421.6	40.7	736	6	CD466140
12	414	40.0	2111	3	AK007808
13	397	38.4	789	6	CD466479
14	391.4	37.8	728	7	CO959203
15	389.4	37.6	683	6	CD535056
16	385.4	37.2	650	6	CD467795
17	384.8	37.2	664	6	CD470054
18	384.6	37.2	673	6	CD466424
19	383	37.0	691	6	CD468594
20	381.6	36.9	654	6	CD466568
21	368.2	35.6	623	6	CD471186
22	364	35.2	749	6	CD468632
23	363.4	35.1	724	6	CD469405
24	355.8	34.4	702	6	CD468196

25	353.8	34.2	692	7	CN786392	CN786392
26	338	32.7	592	6	CD536762	LeukON6_6
27	335.4	32.4	793	6	CD466229	LeukON2_2
28	334.8	32.3	592	6	CD471634	LeukOS6_4
29	331.4	32.0	578	6	CD465152	LeukON1_2
30	325	31.4	581	5	BP300486	BP300486
31	319.4	30.9	576	5	BP295805	BP295805
32	318	30.7	556	6	CD471194	LeukOS5_1
33	316	30.5	885	4	BI082667	LeukOS1_3
34	316	30.4	561	6	CD465288	LeukON1_3
35	313.2	30.3	564	6	CD472150	LeukOS6_1
36	313	30.2	560	6	CD466412	LeukON2_4
37	311.4	30.1	561	6	CD464967	LeukON1_1
38	309.8	29.9	547	6	CD465726	LeukON1_7
39	299	28.9	581	5	BP300273	BP300273
40	297.8	28.8	539	6	CD464212	LeukON4_2
41	296.2	28.6	542	6	CD469002	LeukOS2_1
42	293	28.3	586	6	CD466472	LeukON2_4
43	293	28.3	618	6	CD467329	LeukOS1_3
44	292	28.2	467	7	CR549318	CR549318
45	292	28.2	467	7	CR549318	DKF2p468A

ALIGNMENTS

RESULT 1
BQ892457
LOCUS
DEFINITION
IMAGE:6192227 5', mRNA sequence.
AGENCY: 896 bp mRNA linear EST 16-AUG-2002
Lupski_sympathetic_trunk Homo sapiens cDNA clone

ACCESSION
BQ892457
VERSION
BQ892457.1 GI:22284471

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 896)

AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE
Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLNL13593 ROW: 0 Column: 12

High quality sequence stop: 601.
Location/Qualifiers

1. .896
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6192227"

/sex="male"

/tissue_type="sympathetic trunk"

/dev_stage="adult, 16 yr"

/lab_host="DH10B"

/clone_lib="Lupski_sympathetic trunk"

/notes="Vector: pCMV-Sport6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCAGCGTCCG-3' and 5'-GACTAGTCTAGTCGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life

ORIGIN		Technologies."	
Query Match		71.3%; Score 737.8; DB 5; Length 896;	
Best Local Similarity		96.5%; Pred. No. 6.3e-204;	
Matches 850; Conservative		0; Mismatches 22; Indels 9; Gaps 9;	
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Db	1	ACCAGAGGATGATATGATGCTCTCATAGAGGTGAACCTGGAGAGGATGAGGACAGCA	60
Qy	81	ATGTGCAAGTATGAGCCGAGGACCTCTCAGCCGAGCTGGTGGCCATCACTCTGCTCTGC	140
Db	61	ATGTGACAGTATGAGCCGAGGACCTCTCAGCCGAGCTGGTGGCCATCACTCTGCTCTGC	120
Qy	141	TGTGTTTGTGATCGGTGTCCTGACAAATCTCTGGTGTGCTTATCTCTGGTAAATATAA	200
Db	121	TGTGTTTGTGATCGGTGTCCTGACAAATCTCTGGTGTGCTTATCTCTGGTAAATATAA	180
Qy	201	AGGACTCAACGGGTGAAATATCTATCTTAACTTGGCAGTTTCTAACTTGTGTTT	260
Db	181	AGGACTCAACGGGTGAAATATCTATCTTAACTTGGCAGTTTCTAACTTGTGTTT	240
Qy	261	CTTGCTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGATPCCCATGTGTAAATTTCTCAT	320
Db	241	CTTGCTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGATPCCCATGTGTAAATTTCTCAT	300
Qy	321	TGACTGTACTTCTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCA	380
Db	301	TGACTGTACTTCTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCA	360
Qy	381	AAGTACCTAGTCTTTTGCACAGGGCACTTTTCTCAGCAGGAGGGTGCCCTG	440
Db	361	AAGTACCTAGTCTTTTGCACAGGGCACTTTTCTCAGCAGGAGGGTGCCCTG	420
Qy	441	TGGCATCATTAAGTGTCTGCGATGGGTAAACAGCCATTTCTGGCCACTTTTGCTGAAAT	500
Db	421	TGGCATCATTAAGTGTCTGCGATGGGTAAACAGCCATTTCTGGCCACTTTTGCTGAAAT	480
Qy	501	CGTGGTTTATAAACCCTCAGATGAAGACGAAATACAAGTGTGCATTTAGCAGAACTCC	560
Db	481	CGTGGTTTATAAACCCTCAGATGAAGACGAAATACAAGTGTGCATTTAGCAGAACTCC	540
Qy	561	CTTCTCGCCAGCTGATGAGACATTTCTGGAAGCACTTTCTGACCTTTAAATGAACATTC	620
Db	541	CTTCTCGCCAGCTGATGAGACATTTCTGGAAGCACTTTCTGACCTTTAAATGAACATTC	600
Qy	621	GGTTCTTGTCCT-CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAAAACAC	679
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Qy	680	TAGGTTTCA-GGAGGAGAGGTATAGCCTTTTC-AAGCTTGTTTTTGCCGT-NAATGGTAG	736
Db	661	TAGGTTTCAAGGGAGCAGAAATAGCCTTTTCAAAAGCTTGTTTTGCCATAAATGGTAG	720
Qy	737	TC-TTCTTCTGATGTGGGCGCCCTCAATATTGCAATTTT-CTGTCCACTTTTCAAGA	794
Db	721	TC-TTCTTCTGATGTGGGCGCCCTCAATATTGCAATTTTCTGTCCACTTTTCAAGA	780
Qy	795	ACACTTTC-TCCCTGAGTGACTGCAAGAGCAGCTACAATCTGG-ACAAAAGTGTTCATC	852
Db	781	AACCTTCTTCTGAGTGACTGGCAGAGCAGCTACATCTCTGGAAACAAAAGTGTTCATC	840
Qy	853	ACT-AAACTCATGCCACCAACCACTGCTGCATCAACCCCTC	892
Db	841	ACTAAAATTCATGGCACCCACCACTGCTGCATCAACCCCTC	881
RESULT 2			
CF147784			
LOCUS			
DEFINITION			
CF147784 716 bp mRNA linear EST 25-JUL-2003			
AGENCOURT 14740191 NIH MGC 145 Homo sapiens cDNA clone			
IMAGE:6971947 5', mRNA sequence.			

CF147784	GI:33244052
CF147784.1	EST.
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NIH-MGC	http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Daniela S. Gerhard, Ph.D.	
Office of Cancer Genomics	
National Cancer Institute / NIH	
Bldg. 31 Rm10A07 Bethesda, MD 20892	
Email: c9abps-r@mail.nih.gov	
Tissue Procurement: GPCR Consortium	
CDNA Library Preparation: GPCR Consortium	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Agencourt Bioscience Corporation	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	
http://image.llnl.gov	
Plate: IRB102 row: f column: 06	
High quality sequence stop: 634.	
Location/Qualifiers	
1..716	
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ORIGIN	
Query Match	65.4%; Score 677; DB 7; Length 716;
Best Local Similarity	99.0%; Pred. No. 3.5e-186;
Matches 691; Conservative	0; Mismatches 6; Indels 1; Gaps 1;
QY	1 ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCTATAGAGGTGAACCTG 60
Db	16 ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCTATAGAGGTGAACCTG 75
QY	61 GAGAGCGATGAGCAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCCACTG 120
Db	76 GAGAGCGATGAGCAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCCACTG 135
QY	121 GTGCCATCACTCTGCTCTGTTTGTGATCGGTGCTCTGGACAAATCTCTCTGTTGTG 180
Db	136 GTGCCATCACTCTGCTCTGTTTGTGATCGGTGCTCTGGACAAATCTCTCTGTTGTG 195
QY	181 CTTATCTCTGTTAAATATATAAGGACTCAAAACGGTGGAAAAATATCTATCTTTAAACTTG 240
Db	196 CTTATCTCTGTTAAATATATAAGGACTCAAAACGGTGGAAAAATATCTATCTTTAAACTTG 255
QY	241 GCAGTTTCTAACTGTGTTTCTTGTTCACCTGCCCTTCTGGGCTCATGCTGGGGCGAT 300
Db	256 GCAGTTTCTAACTGTGTTTCTTGTTCACCTGCCCTTCTGGGCTCATGCTGGGGCGAT 315
QY	301 CCCATGTGTAAATTTCTCATTTGACCTGCTCGTGGGCTGTACAGTGAGACATTTTTC 360
Db	316 CCCATGTGTAAATTTCTCATTTGACCTGCTCGTGGGCTGTACAGTGAGACATTTTTC 375

Qy 361 AATTGCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGCAAGGGCAACTTTTTCTCA 420
Db 376 AATTGCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGCAAGGGCAACTTTTTCTCA 435
Qy 421 GCCAGGAGGAGGTGCTGCTGGCATCAATCAAGTGTCTGGCATGGTAAACAGCCATT 480
Db 436 GCCAGGAGGAGGTGCTGCTGGCATCAATCAAGTGTCTGGCATGGTAAACAGCCATT 495
Qy 481 CTGGCCACTTTGCTGCAATTCGTGGTATTAAACCTCAGATGGAAGACCAGAAATACAG 540
Db 496 CTGGCCACTTTGCTGCAATTCGTGGTATTAAACCTCAGATGGAAGACCAGAAATACAG 555
Qy 541 TGTGCAATTAGCAGAACTCCCTCTGCGAGTGTAGAGATTCCTGGAAGCAATTTCTG 600
Db 556 TGTGCAATTAGCAGAACTCCCTCTGCGAGTGTAGAGATTCCTGGAAGCAATTTCTG 615
Qy 601 ACTTTAAAAATGAACATTTCCGTTCTGCTGCTCCCTATTATTATTTTACATTTCTCTAT 660
Db 616 ACTTTAAAAATGAACATTTCCGTTCTGCTGCTCCCTATTATTATTTTACATTTCTCTAT 675
Qy 661 GTGCAAAATGAGAAAACACTAAGTTTCAGGGAGCAGAG 698
Db 676 GTGCAAAATGAGAAAACACT-AGTTTCAGGAAGCAGAG 712

RESULT 3

CD370587/c
LOCUS
DEFINITION
UI-H-FT1-bkc-j-11-0-UI s1 NCI CGAP_Ft1 Homo sapiens CDNA clone
UI-H-FT1-bkc-j-11-0-UI 3', mRNA sequence.
ACCESSION
CD370587
VERSION
CD370587.1 GI:31154677
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 729)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Cloning Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

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1. 729
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Ft1"
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_Ft1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24

ORIGIN

Query Match 61.6%; Score 637.8; DB 6; Length 729;
Best Local Similarity 99.4%; Pred. No. 1e-174;
Matches 661; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 371 TGACTGTGCAAGGTACTAGTGTGTTTTTGCAAGGGCAACTTTTTCTCAGCAGAGGA 430
Db 729 TGACTGTGCAAGGTACTAGTGTGTTTTTGCAAGGGCAAC-TTTTCTCAGCAGAGGA 672
Qy 431 GGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGTAAACGCCATTCTGGCCACTT 490
Db 671 GGGTGCCCTGTGGCATCATTAACAAGTGTCTGGCATGGTAAACGCCATTCTGGCCACTT 612
Qy 491 TGCCTGAATTGCTGTTTATAAACCTCAGATGGAAGACCAGAAATACAAAGTGTGCAATTA 550
Db 611 TGCCTGAATTGCTGTTTATAAACCTCAGATGGAAGACCAGAAATACAAAGTGTGCAATTA 552
Qy 551 GCAGAACTCCCTCTGCGAGCTGATGAGACATTTCTGGAAGCATTTTCTGCAATTA 610
Db 551 GCAGAACTCCCTCTGCGAGCTGATGAGACATTTCTGGAAGCATTTTCTGCAATTA 492
Qy 611 TGAACATTTGCTGTTCTCTCCCTCTATTTTATTTTACATTTCTCTATGTGCAATTA 670
Db 491 TGAACATTTGCTGTTCTCTCCCTCTATTTTATTTTACATTTCTCTATGTGCAATTA 432
Qy 671 GAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTTGTTTGGCGTAA 730
Db 431 GAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTTGTTTGGCGTAA 372
Qy 731 TGGTAGTCTTCTCTGATGTGGCGCCCTACAAATATTGCAATTTTCTGCTGCCACTTTCA 790
Db 371 TGGTAGTCTTCTCTGATGTGGCGCCCTACAAATATTGCAATTTTCTGCTGCCACTTTCA 312
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Db 311 AAGAAACACTTCTCCCTGAGTGACTGCAAGAGACGACTACAATCTGAGCAAAAAGTGTTCACA 252
Qy 851 TCACATAAAGTCTGCGCCACCCACCTGCTGCTGATCAACCCCTCTCTCTGATGCGTTTCTTG 910
Db 251 TCACATAAAGTCTGCGCCACCCACCTGCTGCTGATCAACCCCTCTCTCTGATGCGTTTCTTG 192
Qy 911 ATGGGCAATTTAGCAATACTCTGCGCGCTGTTTCCATCTGCGTAGTAAACCCCACTTC 970
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Qy 971 AACCCAGGGGGAGTCTGCAAGGACATCGAGGGAGAACCTGACCATTTCCACCGAAG 1030
Db 131 AACCCAGGGGGAGTCTGCAAGGACATCGAGGGAGAACCTGACCATTTCCACCGAAG 72

hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus + LPS 3
hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares. Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pTT3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
GGCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

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QY      1031 TGTA 1035
Db      |||||
       71  TGTA 67

RESULT 4
CD520843      720 bp mRNA linear EST 06-JUN-2003
LOCUS      AGENCOURT_14369985 NIH_MGC_191 Homo sapiens cDNA clone
DEFINITION IMAGE:30409698 5', mRNA sequence.
ACCESSION   CD520843
VERSION     CD520843.1 GI:31452561
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 720)
            NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCMI98 row: k column: 19
            High quality sequence stop: 497.

FEATURES             source
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            Site 2: SfiI (ggccgctcgcc); Library is oligo-dT primed
            and directionally cloned. PBMC - Peripheral Blood
            Mononuclear Cells. RNA was pooled from 3/6hour stimulation
            with PMA adn Ionomycin. 5' and 3' adaptors were used in
            cloning as follows: 5' adaptor sequence:
            5'-CATGGCCATTATGGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.69
            kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match      59.7%; Score 617.6; DB 6; Length 720;
Best Local Similarity 97.1%; Pred. No. 8.2e-169;
Matches 629; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      1  ATGCCCAATTACAGCTGGCACAGAGGATGATATGATGTCCTCATAGAGGTGAAGTGC 60
Db      |||||
       65  ATGGCCCAATTACAGCTGGCACAGGATGATATGATGTCCTCATAGAGGTGAAGTGC 124

QY      61  GAGAGCGATCAGGACAGCAATGTGACAAGTATGAGCCGAGGACCTCTCAGCCGAGCTG 120
Db      |||||
       125  GAGAGCGATGAGGACAGCAATGTGACAAGTATGAGCCGAGGACCTCTCAGCCGAGCTG 184

QY      121  GTGCCATCACTCTGCTGCTGTTGTGTTGATCGGTCTCTGGCAATCTCTCTGGTTGTG 180
Db      |||||
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Db      185  GTGCCATCACTCTGCTGCTGTTGTGATCGGTGCTCTGGACAATCTCTCTGGTTGTG 244
QY      181  CTTATCTCGTAAATATATTAAGGACTCAAAACGGTGGAAATATCTATCTTCTAAACTTG 240
Db      245  CTTATCTCGTAAATATATTAAGGACTCAAAACGGTGGAAATATCTATCTTCTAAACTTG 304
QY      241  GCAGTTTCTTAACTTGTGTTTCTTGTGTTTACCCTGCCCTTCTGGGCTCATGCTGGGGCGAT 300
Db      305  GCAGTTTCTTAACTTGTGTTTCTTGTGTTTACCCTGCCCTTCTGGGCTCATGCTGGGGCGAT 364
QY      301  CCATGTGTAAATTTCTCATTTGAGACTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 360
Db      365  CCATGTGTAAATTTCTCATTTGAGACTGTACTTGTGGGCTGTACAGTGAGACATTTTTC 424
QY      361  AATTGCTTCTGACTGTGCAAGGTACTAGTGTGTTTTTGCACAAGGCAACTTTTCTCA 420
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QY      421  GCAGGAGGAGGCTGCCCTGTGCGCATCATTAACAAGTGTCTCTGSCATGGGTAAACAGCCATT 480
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QY      481  CTGGCCACTTTGCTGCAATTCGTGTTTATAAACCTCAGATGGAACACAGAAATACAAG 540
Db      545  CTGGCCACTTTGCTGCAATTCGTGTTTATAAACCTCAGATGGAACACAGAAATACAAG 604
QY      541  TGTGCATTTAGCAGAACTCCCTTCTCCGAGCTGATGAGACATTTCTGGAAGCAATTTCTG 600
Db      605  TGTGCATTTAGCAGAACTCCCTTCTCCGAGCTGATGAGACATTTCTGGAAGCAATTTCTG 664
QY      601  ACTTTAAAAATGAACATTTTCGGTTCCTGTCCTCCCTCTATTTATTTT 648
Db      665  ACTTTAAAAATGAACATTTTCGGTTCCTGTCCTCCCTCTATTTATT 712
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RESULT 5
BI834559      831 bp mRNA linear EST 04-OCT-2001
LOCUS      603089767F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228561 5',
DEFINITION mRNA sequence.
ACCESSION   BI834559
VERSION     BI834559.1 GI:15946109
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 831)
            NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11575 row: f column: 18
            High quality sequence stop: 813.
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        /notes="Organ: pooled pancreas and spleen; Vector:
            pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
            source anonymous pool of spleen and pancreas from 28 yo
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male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.9%; Score 609.8; DB 4; Length 831;
Best Local Similarity 99.4%; Pred. No. 1.6e-166;
Matches 633; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Qy 1 ATGGCCATTACAGCTGGCCAGAGATGAATATGATGCTCATAGAGGGAAGT 60
Db 194 ATGGCCATTACAGCTGGCCAGAGATGAATATGATGCTCATAGAGGGAAGT 253
Qy 61 GAGAGCGATGAGGAGAGCAATGACAAATGATGACGCCAGGCACTCTAGCCAGCTG 120
Db 254 GAGAGCGATGAGGAGAGCAATGACAAATGATGACGCCAGGCACTCTAGCCAGCTG 313
Qy 121 GTGCCATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 314 GTGCCATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
Qy 181 CTATCTCGTAAATATAAAGGACTCAAGCGGTGGAATAATCTATCTTCTAAACTTG 240
Db 374 CTATCTCGTAAATATAAAGGACTCAAGCGGTGGAATAATCTATCTTCTAAACTTG 433
Qy 241 GCAGTTTCTACTGTTGTTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 434 GCAGTTTCTACTGTTGTTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
Qy 301 CCCATGTGTAATATCTCATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 494 CCCATGTGTAATATCTCATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
Qy 361 AATTGCTTCTGATGCAAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 554 AATTGCTTCTGATGCAAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
Qy 421 GCCAGGAGGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
Db 614 GCCAGGAGGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
Qy 480 TCTGCCACATTTG-CCTGAATTCGTGTTTATAAACCTCAGATGGAAGACAGAAATACA 538
Db 674 TCTGCCACATTTG-CCTGAATTCGTGTTTATAAACCTCAGATGGAAGACAGAAATACA 733
Qy 539 AGTGTGATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
Db 734 AGTGTGATTTAGCAGAACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
Qy 599 TGACTTTTAAATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
Db 794 TGACTTTTAAATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830

RESULT 6

CO959196/c 773 bp mRNA linear EST 17-AUG-2004
LOCUS AGENCOURT 30842374 NIH MGC 146 Homo sapiens cDNA clone
DEFINITION IMAGE:7389718 3', mRNA sequence.

ACCESSION CO959196

VERSION CO959196.1 GI:51323776

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 773)

NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: dsgerha@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
Plate: IRB17 row: d column: 08
High quality sequence start: 18
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FEATURES

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multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRBP.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.4%; Score 594.4; DB 7; Length 773;
Best Local Similarity 98.2%; Pred. No. 5.1e-162;
Matches 610; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 414 TTTCTCAGCAGGAGGAGGTCCTGTCGATCATTTACAGATGTCCTGGCATGGTAAAC 473
Db 638 TTTTTCAGCAGAGGAGGTCCTGTCGATCATTTACAGATGTCCTGGCATGGTAAAC 579
Qy 474 AGCCATTCGCGCCACTTTGCTGCTGAATTCGTGGTTTATAAACCTCAGATGGAAGACAGAA 533
Db 578 AGCCATTCGCGCCACTTTGCCAGAAATACGTGGTTTATAAACCTCAGATGGAAGACAGAA 519
Qy 534 ATACAAGTGTGCAATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCA 593
Db 518 ATACAAGTGTGCAATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCA 459
Qy 594 TTTTCTCAGCTTTAAAAATGAACATTTTCGGTTCTTGTCTCTCCCTCTATTTATTTTACATT 653
Db 458 TTTTCTCAGCTTTAAAAATGAACATTTTCGGTTCTTGTCTCTCCCTCTATTTATTTTACATT 399
Qy 654 TCTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCTTTTCAA 713
Db 398 TCTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCTTTTCAA 339
Qy 714 GCTTGTGTTTGGCGTAATGTTAGTGTCTTCTGATGTGGGCGCCCTACATAATTTGCATT 773
Db 338 GCTTGTGTTTGGCGTAATGTTAGTGTCTTCTGATGTGGGCGCCCTACATAATTTGCATT 279
Qy 774 TTTTCTGCTCCACTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCT 833
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Qy 834 GGACAAAGTGTTCACATCACTAACTCATCGCCACCCACCTGCTGCATCAACCTCT 893
Db 218 GGACAAAGTGTTCACATCACTAACTCATCGCCACCCACCTGCTGCATCAACCTCT 159
Qy 894 CTTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGCGCTGTTTCCATCTGCG 953

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Db      158  CCTGTATCGCTTCTTGTATGGGACATTTAGCAATACCTCTGCGCGTGTTCATCTGG 99
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Db      98   TAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAGGCACATCGAGGGAAGAAC 39
Qy      1014 TGACCAATTCACCGAAGTGTA 1034
Db      38   TGACCA-TCCACCGAAGTGTA 19

RESULT 7
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LOCUS      880 bp      mRNA      linear      EST 04-OCT-2001
DEFINITION 603041489F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182006 5',
mRNA sequence.
ACCESSION  BI819787
VERSION     BI819787.1  GI:15931337
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 880)
JOURNAL     NIH-MGC http://mgs.nci.nih.gov/.
COMMENT     National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                    male lung, age 27; and 1 male testis, age 69. Library is
                    oligo-dT primed and directionally cloned (EcoRV site is
                    destroyed upon cloning). Average insert size 1.8 kb,
                    insert size range 1-3 kb. Library is normalized and
                    enriched for full-length clones and was constructed by C.
                    Gruber (Invitrogen). Research Genetics tracking code
                    021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match      50.9%; Score 526.6; DB 4; Length 880;
Best Local Similarity 93.9%; Pred. No. 3.6e-142;
Matches 604; Conservative 0; Mismatches 29; Indels 10; Gaps 5;

Qy      1  ATGCCCAATTACAGCTGGCAGCAGAGGATGAATATGATCTCTCATAGAGTGAAGT 60
Db      239  ATGCCCAATTACAGCTGGCAGCAGAGGATGAATATGATCTCTCATAGAGTGAAGT 298
Qy      61  GAGAGCGATCAGGCAGCAAGTGTGACAACTATGACGCCAGGCAGCTCTCAGCCAGCTG 120
Db      299  GAGAGCGATCAGGCAGCAAGTGTGACAACTATGACGCCAGGCAGCTCTCAGCCAGCTG 358
Qy      121  GTGCCATCACTCTGCTGTGTTTGTGATCGGTGTCTTGACAAATCTCTGTTGTG 180
Db      359  GTGCCATCACTCTGCTGTGTTTGTGATCGGTGTCTTGACAAATCTCTGTTGTG 418
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Qy      181  CTTATCTCTGGTAAATATATAAGAGACTCAAAACGGTGGAAAATATCTATCTTTAAACTTG 240
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Qy      241  GCAGTTTCTAACTTGTGTTTCTTGTCTTACCCCTGCCCCCTTCTGGGCTCATGCTGGGGGCGAT 300
Db      479  GCAGTTTCTAACTTGTGTTTCTTGTCTTACCCCTGCCCCCTTCTGGGCTCATGCTGGGGGCGAT 538
Qy      301  CCCATGTGTAAATTTCTCATTTGGACTGTACTTGGCTGGGCTGTACAGTGAGACATTTTTTC 360
Db      539  CCCATGTGTAAATTTCTCATTTGGACTGTACTTGGCTGGGCTGTACAGTGAGACATTTTTTC 598
Qy      361  AATTGCTTCTGACTGTGCAAGGTACTAGTGTGTTTTCACAAAGGCAACTTTTTTCTCA 420
Db      599  AATTGCTTCTGACTGTGCAAGGTACTAGTGTGTTTTCACAAAGGCAACTTTTTTCTCA 657
Qy      421  GCCAGGAGGAGGTGCCCTGT-GGCATCATTAACAAGTGTCTGGCATGGTAAACAGCCAT 479
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Qy      480  TCTGGCCACTTTGCCCT--GAATTGCGGTTTATAAACTCAGAT--GGAAGACCAAGAAAT 535
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Qy      536  ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGA---GACATTTCTGGAAG 591
Db      778  ACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGATGAGCACCATCTGGAAG 837
Qy      592  CATTTTCTGACTTTTAAAAATGAACATTTCCGTTTCTTGCTCTCC 634
Db      838  CATTTTCTGACTTTTAAAAATGAACATTTCCGTTTCTTGCTCTACC 880

RESULT 8
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LOCUS      750 bp      mRNA      linear      EST 20-OCT-2000
DEFINITION 601449442F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853378 5',
mRNA sequence.
ACCESSION  BE871331
VERSION     BE871331.1  GI:10320107
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 750)
JOURNAL     NIH-MGC http://mgs.nci.nih.gov/.
COMMENT     National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9577 row: c column: 11
            High quality sequence stop: 735.
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                    /clone="IMAGE:3853378"
                    /tissue_type="adenocarcinoma"
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                    Average insert size 1.8 kb. Library constructed by Life
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Technologies. "

ORIGIN

Query Match 45.4%; Score 470.2; DB 2; Length 750;
 Best Local Similarity 95.2%; Pred. No. 1e-125;
 Matches 517; Conservative 0; Mismatches 23; Indels 3; Gaps 3;

QY 1 ATGGCCAAATACACCTGGCAGGATGAATATGATGCTCATAGAGGTGAACCTG 60
 DB 211 ATGGCCAAATACACCTGGCAGGATGAATATGATGCTCATAGAGGTGAACCTG 270

QY 61 GAGAGCGATAGGAGAGATGACAAAGTATGAGCCCGGCACTCTCAGCCAGCTG 120
 DB 271 GAGAGCGATAGGAGAGATGACAAAGTATGAGCCCGGCACTCTCAGCCAGCTG 330

QY 121 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 331 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389

QY 181 CTATCTCTGTAATAATAAAGGACTCAACCGGTGGAAATATCTATCTTCTAAACTTG 240
 DB 390 CTATCTCTGTAATAATAAAGGACTCAACCGGTGGAAATATCTATCTTCTAAACTTG 449

QY 241 GCAGTTTCTTAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 300
 DB 450 GCAGTTTCTTAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 509

QY 301 CCCATGTGTAATAATCTCATTTGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
 DB 510 CCCATGTGTAATAATCTCATTTGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 568

QY 361 AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420
 DB 569 AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 627

QY 421 GCCAGGAGGAGGTCCTGTCGTCATCTTCAAGTGTCTGTCGTCATCTGTCGTCGTCAT 480
 DB 628 GCCAGGAGGAGGTCCTGTCGTCATCTTCAAGTGTCTGTCGTCATCTGTCGTCGTCAT 687

QY 481 CTGCGCACTTGTGCTGAATTCGTGTTTATATAAATCTCAGATGGAAGCAGCAATACAAG 540
 DB 688 CTGCGCACTTGTGCTGAATTCGTGTTTATATAAATCTCAGATGGAAGCAGCAATACAAG 747

QY 541 TGT 543
 DB 748 TGT 750

RESULT 9
 CD468404
 LOCUS
 DEFINITION LeukoS3_3_F11.bl A025 mRNA linear EST 04-JUN-2003
 Equis caballus cDNA clone LeukoS3_3_F11_A025 3', mRNA sequence.

ACCESSION CD468404
 VERSION
 KEYWORDS
 SOURCE Equis caballus (horse)
 ORGANISM Equis caballus

REFERENCE 1 (bases 1 to 768)
 AUTHORS Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.
 TITLE An EST database from equine (Equis caballus) stimulated peripheral blood leukocytes
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: LeukoS3_3_F11.g1 A025
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210

Email: mmpratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
 Seg primer: Sug3 (CGACCTGCAGTCGAGCACA)
 POLYA=No.

FEATURES
source

Location/Qualifiers
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ORIGIN

Query Match 42.6%; Score 440.4; DB 6; Length 768;
 Best Local Similarity 76.9%; Pred. No. 5.4e-117;
 Matches 569; Conservative 0; Mismatches 156; Indels 15; Gaps 2;

QY 296 GCGATCCCATGTGTAAATTTCTCATTTGAGCTGTACTTCGTGGGCTGTACAGTGAGACAT 355
 DB 1 GCGACCCCAAGTGTCAAAATTTCTGGTAGCGCTCTCTCTGTAGGCTATACAGTGAGGAT 60

QY 356 TTTTCAATTCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAGGGCAACTTTT 415
 DB 61 TTTTCAATTCCTTCTGACTGTGCAAGGTGCTGTGTTTTCACAAGGGCAACTTTT 120

QY 416 TCTCAGCCAGGAGGAGGTCCTGTCGTCATCTTCAAGTGTCTGCGCATGGGTAAACAG 475
 DB 121 CCTC-----GGTCCCGCGGCGCATCATCAAGTGTCTGCGCATGGGGAATAG 168

QY 476 CCATTCTGGCCACTTTTCCCTGAAATTCGTGGTTTATAAACCTCAGATGGAAGCAGCAAAAT 535
 DB 169 CTATTCTGGTCTCTTTGCCCTGAAATTTGGTGTGTTTACGAACCCACAGGTGGGAAGCCAGAAAT 228

QY 536 ACAAGTGTGCATTTAGCAGAACTCCCTTCTTCTGCGCAGCTGATGAGACATTCGGAAGCAT 595
 DB 229 ATAAAGTCTTCTTTGGCAACCTCATTTCTGCGCGCTGATGAGACGCTTCTGGAAGCAT 288

QY 596 TTCTGACTTTAAAATGAACATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 655
 DB 289 TTCTGACTTTGAGGACGAAATTTTGGAGTCTCTTTTCCCACTGTTGTTTATATATTT 348

QY 656 TCTATGTGCAATAGAGAAAACTAAGGTTTCAGGAGGAGCAGAGGTATAGCTTTTCAAGC 715
 DB 349 GCTATGTGCAATAGAGAAAACTAAGGTTTCAGGAGGAGGAGATATGATCTTTTCAAGC 408

QY 716 TTGTTTTTGGCGTAATGGTAGTCTTCTTCTGATGTGGGCGCCCTACAATATTTCATTTT 775
 DB 409 TTGTTTTTGGCGTAATGGTAGTCTTCTTCTGATGTGGGCGCCCTACAATATTTCATTTT 468

QY 776 TCCTGTCCACTTTCAAGAAACATTTCTTCTTCTGAGTGTGAGTGTGAGGAGGAGCTACAACTGG 835
 DB 469 GCTTATCCACTTTCAAGAACTACTTCTTCTGCTGCAAGATTTCAGGAGCAGCTACAACTGG 528

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QY 836 ACAAAGTGTTCATCACTAAACTCATCGCCACCCCACTGCTGCATCAACCCCTCTCC 895
Db 529 ACAAAGTGTTCATCACTAAACTCATCGCCACCCCACTGCTGCATCAACCCCTCTCC 588
QY 896 TGTATGGTTTCTTGATGGACATTTAGCAATAACCTCTGCCGCTGTTTCCATCTCGTA 955
Db 589 TCTACGTGCTTCTTGACAAGAAATTTAGGAAACACCTCTGCCGCTTGGCCATCTG--G 645
QY 956 GTAAACCCCACTTCAACCCAGGGGCGAGTCTGCACAGGCACATCGAGGGAAGACCTG 1015
Db 646 GTAAACGCTCCACCGCAACCACTGAGAGATGCGACACGTCACACGGGGGAAGACAG 705
QY 1016 ACCATTCCACCGAAGTGTA 1035
Db 706 ACCTTTCCTGCTGAATGCAA 725

RESULT 10
BG386374
LOCUS 602455580F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4584043 5',
DEFINITION mRNA sequence.
ACCESSION BG386374
VERSION BG386374.1 GI:13279820
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1035)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1308 row: o column: 20
High quality sequence stop: 526.
Location/Qualifiers
1. .1035
/organisms="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4584043"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/notes="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

Query Match 41.8%; Score 433; DB 4; Length 1035;
Best Local Similarity 93.6%; Pred. No. 8.8e-115;
Matches 484; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

QY 1 ATGCCCAATTACAGCTGGCCACGAGATGATATGATCTCTCTCATAGAGGTGAAGCTG 60
Db 240 ATGCCCAATTACAGCTGGCCACGAGATGATATGATCTCTCATAGAGGTGAAGCTG 299
QY 61 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCCGGCGCACTCTCAGGCCAGCTG 120
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Db 300 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCCGGCGCACTCTCAGGCCAGCTG 359
QY 121 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGCTCGACAAATCTCTCTGTTGTG 180
Db 360 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGCTCGACAAATCTCTCTGTTGTG 419
QY 181 CTTATCTCTGTTAAATATATAAGGACTCAAAACGGGTGAAAAATATCTATCTTCTAAACTTG 240
Db 420 CTTATCTCTGTTAAATATATAAGGACTCAAAACGGGTGAAAAATATCTATCTTCTAAACTTG 479
QY 241 GCAGTTTCTTAACCTGTTTCTTGTGTTAACCCCTGCTTCTGGGCTCATGCTGGGGCGAT 300
Db 480 GCAGTTTCTTAACCTGTTTCTTGTGTTAACCCCTGCTTCTGGGCTCATGCTGGGGCGAT 539
QY 301 CCCATGTGTAAATTTCTCATTTGGACTGTACTTGGGGCTGTACAGTGAGACATTTTTC 360
Db 540 CCCATGTGTAAATTTCTCATTTGGACTGTACTTGGGGCTGTAAACAGTGAGACATTTTTC 599
QY 361 AATTGCTTTCTGACTGTGCAAAGGTACCT-AGTGTGTTTTTGCAACAGGGCAACTTTTTTCTC 419
Db 600 AATTGCTTTCTGACTGTGCAAAGGTACCTAATGTAGTTGCAACAGGTGCACCTTTTTTCTC 659
QY 420 AGCCAGGAGGAGGGTCCCTGTGGCATCAATTACA-AGTGTCTCTGGCATGGGTAAACGCCA 478
Db 660 AGCCAGGAGGAGGGTCCCTGTGGCATCAATTACACAGTGTCTCTGGCATGGGTAAACGCCA 719
QY 479 TTC-TGGCCACTTTCCTGCTGAATTCGGTGTATTAAC 514
Db 720 TTCTTGGCCACTTTCCTGCTGAATTCGGTGTATTAAGC 756

RESULT 11
CD466140
LOCUS LeukoN2_2_B11.b1_A024 Unstimulated peripheral blood leukocytes N2
DEFINITION Equus caballus cDNA clone LeukoN2_2_B11_A024 3', mRNA sequence.
ACCESSION CD466140
VERSION CD466140.1 GI:31387408
KEYWORDS EST.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
REFERENCE 1 (bases 1 to 736)
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Eukaryota; Eutheria; Perissodactyla; Equidae; Equus.
JOURNAL An EST database from equine (Equus caballus) unstimulated
peripheral blood leukocytes
COMMENT Unpublished (2003)
Other ESTs: LeukoN2_2_B11.g1_A024
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp Pratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicine, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
Phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=No.
Location/Qualifiers
1. .736
/organism="Equus caballus"
/mol_type="mRNA"
/strain="thoroughbred"
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FEATURES
source


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/db_xref="taxon:9796"
/clone="Leukon2_2_B11_A024"
/sex="male"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH108-T1 phage-resistant E. coli"
/clone_lib="Unstimulated peripheral blood leukocytes N2"
/notes="Organ: circulatory system; Vector: pME18S-FL3;
Site 1: XhoI; Site 2: XhoI; The library was prepared from
polyA+ RNA from unstimulated equine peripheral blood
leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."
ORIGIN
Query Match 40.7%; Score 421.6; DB 6; Length 736;
Best Local Similarity 77.4%; Pred. No. 1.7e-111;
Matches 543; Conservative 0; Mismatches 144; Indels 15; Gaps 2;
Qy 334 GTGGCCCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAGGTACCTAGTG 393
Db 1 GTAGCCCTATACAGTGAGGCATTTTCAATGCCCTTCTGACTGTGCAAGGTGCTGTG 60
Qy 394 TTTTGGCAAGGGCAACTTTTTCAGCCAGGAGGGTGCCTGTGGCATCATTAACA 453
Db 61 TTTTGTGACATGGAGACGCTTTCCTC-----GGTGCCCGGTGGCATCATCA 108
Qy 454 AGTGCTCGGATGGGTAAACGCCATCTGCGCCACTTTGCTGTAATTCGTGGTTTATAA 513
Db 109 AGTGCTCGGATGGGGAATAGTATTCGTCTCTTTGCTGTAATTCGTGGTTTACGA 168
Qy 514 CCTCAGATGGAAGACACAGAAATACAAAGTGTGCATTTAGCAGACTCCCTCTGCCAGCT 573
Db 169 CCACAGGTGGAAGCCAGAAATATAAGTCTCTTTGGCAACCTCATTTCTGCCGCT 228
Qy 574 GATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTTCGTTCTTCCTC 633
Db 229 GATGAGACGTTCTGGAAGCATTTTCTGACCTTGAGGACGAACATTTTGGGACTTCTTTTC 288
Qy 634 CCCCTATTATTATTACATTTCTATGTGCATATGAGAAACACTTAAGGTTTCAGGAG 693
Db 289 CCACGTGTTTGTATATTTTGTATGTGCAATGAGAAACAAATGAAGATTTTGGGAAA 348
Qy 694 CAGAGGTATAGCTTTTCAAGCTTGTTTTTCGGTAATGTAGTCTTCTCTCATGTGG 753
Db 349 AGGAGATATGATCTTACAGCTTGTTTTCCGTAATGTGTGTTTCTTCTCATGTGG 408
Qy 754 GCGCCCTACAAATATGCAATTTTCTGTCCACTTTTCAAAGAACACTTCTCCCTGAGTGAC 813
Db 409 GGACCCCTACAAATGTTGCATTTTGTCTATCCACTTTCAAAGACTACTTCTGCTGCAAGAT 468
Qy 814 TGCAGAGCAGCAGTACATCTGCAAAAAGTGTTCACATCACTAACTCATGCCACACACC 873
Db 469 TGCAGGACAGCAGTACAACTGCAAAAAGTGTTCACATCATGAAATCGTCGCCACACACC 528
Qy 874 CACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTC 933
Db 529 CACTGCTGTGCAACCCGCTCTCTACGTGTTCTTGCAAGGAATTTAGGAACACCTC 588
Qy 934 TGCCGCTGTTTCCATCTCGGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCACAA 993
Db 589 TGCCGCTTGGCCATCTG---GGTAACGCTCCACCGCAACCCACTGAGAGATGCGCACCA 645
Qy 994 GGCAATCGAGGGGAAGAACCTGACCATTCACCCAGGAAGTGA 1035
Db 646 CGTACACCGGGGGAAGAACACGACCTTTCTGCTGAAATGCAA 687

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RESULT 12

AK007808

LOCUS

2111 bp mRNA linear HTC 03-APR-2004

DEFINITION

Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810047105 product:chemokine (C-C) receptor 1,-like 2, full insert sequence.

ACCESSION

AK007808.1 GI:12841594

VERSION

HTC; CAP trapper.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

1 Carninci,P. and Hayashizaki,Y.

REFERENCE

High-efficiency full-length cDNA cloning

AUTHORS

Meth. Enzymol. 303, 19-44 (1999)

JOURNAL

99279253

MEDLINE

10349636

REFERENCE

2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Sugahara,K.,

AUTHORS

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to

JOURNAL

prepare full-length cDNA libraries for rapid discovery of new genes

MEDLINE

Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE

3 Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P.,

AUTHORS

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

JOURNAL

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

MEDLINE

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,

REFERENCE

Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,

AUTHORS

Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,

TITLE

Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

JOURNAL

RIKEN integrated sequence analysis (RISA) system--384-format

MEDLINE

sequencing pipeline with 384 multicapillary sequencer

REFERENCE

Genome Res. 10 (11), 1757-1771 (2000)

AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the

TITLE

FANTOM Consortium.

JOURNAL

Functional annotation of a full-length mouse cDNA collection

MEDLINE

Nature 409, 695-690 (2001)

REFERENCE

5 The FANTOM Consortium and the RIKEN Genome Exploration Research

AUTHORS

Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation

JOURNAL

of 60,770 full-length cDNAs

MEDLINE

Nature 420, 563-573 (2002)

REFERENCE

6 (bases 1 to 2111)

AUTHORS

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,

JOURNAL

Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,

MEDLINE

Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,

REFERENCE

Hiraoka,T., Hori,P., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,

AUTHORS

Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,

JOURNAL

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,

Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,

Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,

Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,

Suzuki,H., Tagami,M., Tagawa,A., Takahashi,P., Tanaka,T.,

Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,

Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp.

URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,

Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.jp/) for further

details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGG).

FEATURES

Location/Qualifiers
1..789
/organism="Bqus caballus"
/mol_type="mRNA"
/strain="thoroughbred"
/db_xref="taxon:9796"
/clones="Leukon2_4_E11_A024"
/sex="male"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Unstimulated peripheral blood leukocytes N2"
/note="Organ: circulatory system; Vector: pME18S-FL3; Site1: XhoI; Site2: XhoI; The library was prepared from polyA+ RNA from unstimulated equine peripheral blood leukocytes isolated from a healthy adult horse. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN
Query Match 38.4%; Score 397; DB 6; Length 789;
Best Local Similarity 76.1%; Pred. No. 2.7e-104;
Matches 555; Conservative 0; Mismatches 140; Indels 34; Gaps 4;

Qy 1 ATGCCCAATTACAGCTGGCCACAGAGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
Db |||||
Qy 77 ATGGCTAATTACAGCTCCACACAGAGATGAATATGATGTCCTCATAGAGAGCATCTG 136
Db |||||
Qy 61 GAGAGCATGAGGAGGAGGATGACAGATGATGACGCCAGGACATCTCAGCCAGCTG 120
Db |||||
Qy 137 AATA---ACAAGATAGAACAAATGGACAAATATGACCAAGATTCCTCAGCCAAGCTG 193
Db |||||
Qy 121 GTGCCATCAGCTCTGCTGCTGTTGTGATCGGTGCTCGTGGACAAATCTCCTGGTGTG 180
Db |||||
Qy 194 GTGCTGCTCTACAGAGTGTGTTCTGCTCGTCTCTGGACATCTGTTGGTGTG 253
Db |||||
Qy 181 CTTATCCTGTAATAAATAAGGACTCAACGCTGGAAATATCTATCTTCTAAACCTG 240
Db |||||
Qy 254 CTTATCCTGTAATAAATAAGGACTCAACGCTGGAAATATCTATCTTCTAAACCTG 313
Qy |||||
Qy 241 GCAGTTTCTACTGCTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTG----- 292
Db |||||
Qy 314 GCAGTTTCTAAATTTGTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGCCCCAT 373
Qy |||||
Qy 293 -----GGGCGGATCCCATGTAATAATCTCATTTGACATGATCTCGTGGGCTG 342
Db |||||
Qy 374 GGGGGGATTCGCGGAGCCCAAGTGTCAATTTCTGGTGGCTCTCTCTGTAGGCTA 433
Qy |||||
Qy 343 TACAGTGAGACATTTTCAATGCTGCTGCTGCTGCAAGGTACCTAGTGTGTTTTCAC 402
Db |||||
Qy 434 TACAGTGAGGCAATTTTCAATGCTGCTGCTGCTGCAAGGTGCTGTTTTCAC 493
Qy |||||
Qy 403 AAGGCAACTTTTCTCAGCCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 462
Db |||||
Qy 494 ATGAGAGCGCTTTCCTC-----GGTGGCGCTGGCATCATCAAGTGTCTG 541
Qy |||||
Qy 463 GCATGGGTAAACAGCACTTTCGGCCACTTTCGCTGAATTCGTGGTGTATTAACCTCAGATG 522
Db |||||
Qy 542 GCATGGGGAATAGCTATTCGTGCTCTCTTGGCTGAATTTGTTTTCAGAACCAAGCTG 601
Db |||||
Qy 523 GAAGACCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAGACA 582
Db |||||

Db |||||
Qy 602 GAAAGCCAGAAATATAAGTGTCTTTTGGCAAACTCATTTCTCGCGGCTGATGAGACG 661
Db |||||
Qy 583 TTCTGGAAGCATTTTCTGACCTTAATAATGAACATTTGGTCTTGTCTCCCTATTT 642
Db |||||
Qy 662 TTCTGGAAGCATTTTCTGACCTTGAAGCAGCAATTTTGGACATCTTTTCCCTGTT 721
Qy |||||
Qy 643 ATTATTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGTTTCAGGAGCAGAGGTAT 702
Db |||||
Qy 722 GTTTTATATTTTGTCTATGCGAATGAG-AAAACAATAAGATTTGGGAAAAGGAGATAT 780
Qy |||||
Qy 703 AGCCTTTTC 711
Db |||||
Qy 781 GATCTTTAC 789

RESULT 14
CO959203
LOCUS
DEFINITION
AGENCY 30842774 NIH MGC 146 Homo sapiens cDNA clone
IMAGE:7389718 5', mRNA sequence.
ACCESSION
CO959203
VERSION
CO959203.1 GI:51323783
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 728)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcgbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB17 row: d column: 08
High quality sequence start: 68
High quality sequence stop: 638.

FEATURES
source
1..728
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7389718"
/tissue_type="mixed"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 146"
/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image_rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 37.8%; Score 391.4; DB 7; Length 728;
Best Local Similarity 98.5%; Pred. No. 1.1e-102;
Matches 395; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGCAATTACAGCTGGCCAGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
Db |||||

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Db      3  ATGCCCAATTACACGCTGGCACAGAGGAAGAATATGATGTCCTCATAGAAAGTGAACCTG 62
Qy      61  GAGAGCATGAGGAGAGCAATGTGACAAGATGACGCCAGGCACTCTCAGCCAGCTG 120
Db      63  GAGAGCATGAGGAGAGCAATGTGACAAGATGACGCCAGGCACTCTCAGCCAGCTG 122
Qy      121  GTGCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db      123  GTGCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182
Qy      181  CTTATCTCGTAAATATAAGAGACTCAAAAGCGGTGGAATAATATCTATCTTCTAAACTTG 240
Db      183  CTTATCTCGTAAATATAAGAGACTCAAAAGCGGTGGAATAATATCTATCTTCTAAACTTG 242
Qy      241  GCAGTTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db      243  GCAGTTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302
Qy      301  CCATGTTGTAATAATCTCAATTGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db      303  CCATGTTGTAATAATCTCAATTGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 362
Qy      361  AATTGCTCTTCTGACTGTGCAAGTACCTAGTGTGTTTGTCA 401
Db      363  AATTGCTCTTCTGACTGTGCAAGTACCTAGTGTGTTTGTCA 403
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RESULT 15

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CD535056      683 bp mRNA linear EST 10-JUN-2003
LOCUS      Leukon5_3 C06.bi A027 Unstimulated peripheral blood leukocytes N5
DEFINITION      Equus caballus cDNA clone Leukon5_3_C06_A027 3', mRNA sequence.
ACCESSION      CD535056
VERSION      CD535056.1 GI:31577471
KEYWORDS      EST.
SOURCE      Equus caballus (horse)
ORGANISM      Equus caballus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
              1 (bases 1 to 683)
REFERENCE      Vandenplas,M., Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S.,
AUTHORS      Moore,J.N., Liang,C., Sun,F., Sullivan,R., Shah,M. and Pratt,L.H.
              An EST database from equine (Equus caballus) unstimulated
              peripheral blood leukocytes
              Unpublished (2003)
JOURNAL      Other_ESTs: Leukon5_3_C06.g1_A027
COMMENT      Contact: Cordonnier-Pratt MM
              Laboratory for Genomics and Bioinformatics
              The University of Georgia, Department of Plant Biology
              Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
              Tel: 706 542 1860
              Fax: 706 583 0210
              Email: mmpratt@uga.edu
              Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
              the Human Genome Center, University of Tokyo Institute of Medical
              Science; tissue and RNA were prepared in the Department of Large
              Animal Medicine, University of Georgia; sequencing done in the
              Laboratory for Genomics and Bioinformatics, University of Georgia.
              Sequence ends have been trimmed to exclude vector and regions below
              Phred quality 16. Three-prime sequences are presented as their
              reverse complement and have been trimmed to exclude polyA.
              Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
              POLYA=Yes.
```

FEATURES

```
source      Location/Qualifiers
              1..683
              /organism="Equus caballus"
              /mol_type="mRNA"
              /strain="Dartmoor Pony"
              /db_xref="taxon:9796"
              /clone="Leukon5_3_C06_A027"
              /sex="male"
              /tissue_type="blood"
              /cell_type="leukocytes"
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Search completed: June 18, 2005, 12:07:55
Job time : 3963.26 secs

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/lab_host="DH10B-Ti phage-resistant E. coli"
/clone_lib="Unstimulated peripheral blood leukocytes N5"
/notes="Organ: circulatory system; Vector: pME18S-FL3,
Site 1: XhoI; Site 2: XhoI; The library was prepared from
polyA+ RNA from unstimulated equine peripheral blood
leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG). XhoI excises the cDNA insert."
```

ORIGIN

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Query Match      37.6%; Score 389.4; DB 6; Length 683;
Best Local Similarity 76.5%; Pred. No. 4.2e-102;
Matches 509; Conservative 0; Mismatches 141; Indels 15; Gaps 2;

Qy      371  TGACTGTGCAAAAGGTACCTAGTGTGTTTTGCAAGGGCAACTTTTCTCAGCCAGGAGGA 430
Db      1  TGACTGTGCAAAAGGTGCTGCTGCTGTTTTTGACATGGAGACGCTTTCCTC----- 49
Qy      431  GGGTGCCCTGTGGCATCATTAAGTGTCTCTGGCATGGGTAAAGCCATCTTGGCCACTT 490
Db      50  -GGTGCCCGCTGGCATCATCAAGGTGTCTGGCAGGGGNAATAGCTATTTCTGCTCTCT 108
Qy      491  TGCCTGAATTCGTGGTGTATATAAACCTCAGATGGAAGACCAGAAATACAAAGTGTGCA 550
Db      109  TGCCTGAATTCGTGTGTTTTAGAACACACAGGTGGAAAGCCAGAAATATAAGTGTCTT 168
Qy      551  GCAGAACTCCCTTCTGCGCAGCTGATGACATTTCTGGAAGCATTTTCTGACTTTTAAAA 610
Db      169  GCAAACTCATTTCTGCGCGCTGATGAGACGTTCTGGAAGCATTTTCTGACCTTGAGGA 228
Qy      611  TGAACATTTCCGTTCTTGTCTCCCTCCCTATTTATTTTACATTTCTCTATGTGCAATGA 670
Db      229  CGAACATTTTGGACTTCTTTTCCCACTGTTTTTATATCTTTGTTATCTATGTCGAATGA 288
Qy      671  GAAAAACACTAAGGTTTCAGGGAGCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTTGCGGTAA 730
Db      289  GAAAAACATAGGATTTGGAAAAAGAGATATGATCTTTTACAAGCTTGTGTTTTGCGGTAA 348
Qy      731  TGGTAGTCTTCTCTTGTGATGTGGGGCCCTACAATATTTGCAATTTTCTGTCACATTTCA 790
Db      349  TGGTTGTTTTTCTTCTGATGTGGGGACCTACAAATGTTGCACTTTGCTTTATCCACTTTCA 408
Qy      791  AAGAACACTTCTCCCTGAGTGTGCTCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACA 850
Db      409  AAGACTACTTCTGCTGCAAGACTTGAGGCAAGCTACAACTTGGACAAAGTGTTCACA 468
Qy      851  TCACTAAACTCATCGCCACACCCACTGCTGCATCAACCCCTCTCTCTGTATGGCTTTCTTG 910
Db      469  TCATGAATATCGTGGCCACCACCCACTGCTGTGTGTCACCCCGCTCTCTACGTGCTTTTG 528
Qy      911  ATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTGGGTAGTAAACCCCACTTC 970
Db      529  ACAAGGAATTTAGAAAAACCTCTGCGCTTGGCCATCTG---GGTAACGCTCCACCGC 585
Qy      971  AACCCAGGGGCGAGTCTGCACAAAGGCACATCGAGGGGAAGAACTGACCATTTCCACCGAAG 1030
Db      586  AACCCCATGAGATGCGCACCACCGTACACCGGGGGAAGAACACGACCTTTTCTGCTGAAA 645
Qy      1031  TGTAA 1035
Db      646  TGCNA 650
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QY 781 TCACCTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 840
Db 856 TCACCTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 915
QY 841 AGTGTTACACATCACTAAACTCATCGCCACCAACCACCTGCTGTCATCAACCCCTCTCCTGTAT 900
Db 916 AGTGTTACACATCACTAAACTCATCGCCACCAACCACCTGCTGTCATCAACCCCTCTCCTGTAT 975
QY 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCGCTGTTTCCATCTGCGTAGTAAC 960
Db 976 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGCGCTGTTTCCATCTGCGTAGTAAC 1035
QY 961 ACCCCACTTCAACCC 975
Db 1036 ACCCCACTTCAACCC 1050

RESULT 4
US-09-655-308
; Sequence 308, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 308:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGNOT10
; CLONE: 1378524
US-09-023-655-308

Query Match 31.58; Score 326.4; DB 4; Length 620;
Best Local Similarity 99.74; Pred. No. 1.1e-96;
Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 708 TTTCAAGCTGTTTTCGCCGTAATGGTAGTCTTCTCTCATGTGGGCGCCCTACAATAT 767
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Db 5 TTTCAAGCTGTTTTCGCCATAATGGTAGTCTTCTCTCTGATGTGGGCGCCCTACAATAT 64
QY 768 TGCATTTTTCCTGTCACATTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTA 827
Db 65 TGCATTTTTCCTGTCACATTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTA 124
QY 828 CAATCTGGACAAAGAGTGTTCACATCACTAAACTCATCGCCACCAACCACCTGCTGCAATCAA 887
Db 125 CAATCTGGACAAAGAGTGTTCACATCACTAAACTCATCGCCACCAACCACCTGCTGCAATCAA 184
QY 888 CCCTCTCCCTGTATGCGCTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGGCTGTTTCCA 947
Db 185 CCCTCTCCCTGTATGCGCTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGGCTGTTTCCA 244
QY 948 TCTGCGTAGTAAACCCGACCTTCAACCCAGGGGGAGTCTGCACAAAGGCACATCGAGGGA 1007
Db 245 TCTGCGTAGTAAACCCGACCTTCAACCCAGGGGGAGTCTGCACAAAGGCACATCGAGGGA 304
QY 1008 AGAACCTGACCATTTCCACCCGAAAGTGTA 1035
Db 305 AGAACCTGACCATTTCCACCCGAAAGTGTA 332

RESULT 5
US-09-517-605-8
; Sequence 8, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-517-605-8

Query Match 22.54; Score 233; DB 3; Length 1059;
Best Local Similarity 56.84; Pred. No. 9.6e-66;
Matches 531; Conservative 0; Mismatches 365; Indels 39; Gaps 4;

QY 54 TGAACCTGGAGAGCGATGAGCGAGCAAGTGACAAAGTATGACGCCAGGCACCTCTCAGC 113
Db 30 TGACATCGATTATGATACATCGAGGCCCTGCCAAAAAATCAATGTGAAGCAATCGCAGC 89
QY 114 CCAGCTGGTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCTCTGGACAATCTCCT 173
Db 90 CCGCCTCTCTGCTCCACTCTACTCACTGGTGTTCATCTTTGGTTTGTGGCAACATGCT 149
QY 174 GGTGTGCTTATCCTGGTAAATATAAAGGACTCAAAACGGGTGGAAAAATATCTATCTTCT 233
Db 150 GGTATCTCTCGTCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCT 209
QY 234 AAACCTGGCAGTTTCTAACTTGTTTCTTGTGTTTCTTACCTGCCCTCTGGGCTCA----- 287
Db 210 CAACCTGGCCATCTCTGACCTGTTTCTTCTTCTTACTGTCCCTCTGGGCTCACTACGC 269
QY 288 -----TGCTGGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCGT 335
Db 270 TGTGCGCCAGTGGGACTTTTGGAAATACATGTGCAACTTTGACAGGGCTCTATTAT 329
QY 336 GGGCCTGTACAGTGAGACATTTTCAATTTGCTTCTGATCTGTGCAAGAGGTACCTAGTGT 395
Db 330 AGGCTTCTTCTCTGGAATCTTCTTCTATCATCTCTCTGACAAATCGATAGATACCTAGCTAT 389
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QY 396 TTTGCACAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTAAG 455
Db 390 CGTCCATGCTGTGTGCTTTTAAAGCC---AGGACGGTCACTTTGGGGTAGTGAAG 446
QY 456 TGTCTGGCATGGGTAAACAGCCATCTCTGGCCACCTTTGCTGAAATCGTGGTTTATAAAC 515
Db 447 TGTGATCACTTGGGTGGTGTGTGTGATCTCTCCAGGAATCATCTTTACCATC 506
QY 516 TCAGATGGAGACAGAAATACAAAGTGTGCATTTAGAGAACTCCCTTCTGCGAGCTGA 575
Db 507 TCAAAAGAGAGGCTTCTCATTAACCT-----GCAGCTCTCATTTTCCATACAGTCA 557
QY 576 TGAGACATCTCGAGACATTTCTGACTTTTAAATGAACATTTCCGTTCTTGTCTCC 635
Db 558 GTATCAATTTCTGGAGAAATTTCCAGACATTAAGATAGTATCTTTGGGGCTGTCTGCC 617
QY 636 CCTATTATTTTACATTTCTCTATGTGCAATGAGAAACACTAA-----GGTT 686
Db 618 GCTGCTTGTGATGTCATCTGCTACTCGGAATCTTAAATCTGCTTGGTGTGAAA 677
QY 687 CAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCGTAAATGGTAGTCTTCTTCT 746
Db 678 CGAGAGAGAGGACAGGCGTGTAGGCTTATCTTCAACCATCATGATTTGTTATTTTCT 737
QY 747 GATGTGGGCGCTTACAAATATGCAATTTTCTGTGCACTTTTCAAGAACACTTCTCCCT 806
Db 738 CTTCTGGGCTCCCTTACAAATTTGCTTCTCTGAAACACCTTCCAGGAATTTCTTTGGCCT 797
QY 807 GAGTGACTGCAAGAGCAGCTACATCTGGAAGGTTTCAACATCACTAACTCATCGC 866
Db 798 GAATAATTGACAGTCTTAAACAGTTTGAACCAAGCCATGAGGTGACAGACTCTTGG 857
QY 867 CACCACCACTGTGTCATCAACCTCTCTGTATGCTTTTGTGATGGGACATTTAGCAA 926
Db 858 GATGAGCACTGTGTCATCAACCCATCATCTATGCTTTGTTGGGAGAGTTTCAAAA 917
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RESULT 6

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US-08-771-276-19
; Sequence 19, Application US/08771276
; Patent No. 6797811
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicki L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,276
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6797811and, Greta B.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300

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; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1056
; US-08-771-276-19

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Query Match 22.5%; Score 233; DB 4; Length 1059;
Best Local Similarity 56.8%; Pred. No. 9.6e-66;
Matches 531; Conservative 0; Mismatches 365; Indels 39; Gaps 4;

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QY 54 TGAACCTGAGAGCGATGAGCGAGAGCAATGTGACAGTATGACGCCAGGCACTCTCAGC 113
Db 30 TGACATCGATTTATTATACATCGGAACCTCGCAAAATCAATGTGAAACAAATCGCAGC 89
QY 114 CCAAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCTCGGACAAATCTCCT 173
Db 90 CCGCTCTGCTCGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 149
QY 174 GGTGTGCTTATCCTGGTAAATATATAAGGACTCAAAACGGTGGAAATATCTATCTTCT 233
Db 150 GGTGCTCTCATCTGATATACTGCAAAAGGCTGAAAGCATGACTGACATCTACCTGCT 209
QY 234 AAACCTGGGAGTTTCTAACTGTTGTTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 292
Db 210 CAACCTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269
QY 293 -----GGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGCT 335
Db 270 TGTGCTCCAGTGGGACTTTGGAAATACAAATGTGCTCAACTCTTGACAGGGCTCTATTATAT 329
QY 336 GGGCTCTGACAGTGAGACATTTTTCATATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
Db 330 AGGCTTCTCTCTGGAATCTTCTTCTCATCTCTCTGCAAACTGATAGGTACCTGGCTAT 389
QY 396 TTTGCAACAGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTAAG 455
Db 390 CGTCCATGCTGTGTTTCTTAAAGCC---AGGACAGTCACTTTGGGGTGGTGAAG 446
QY 456 TGTCTGGCATGGGTAAACAGCCATCTGCGCACCTTTGCTGAAATTCGTGGTTTATAAAC 515
Db 447 TGTGATCACTTGGGTGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 506
QY 516 TCAGATGGAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGAGCTGA 575
Db 507 TCAGAGAGAGAGGCTTCTCATTTACACT-----GCAGCTCTCATTTTCCATACAGTCA 557
QY 576 TGAGACATCTCGAAGCATTTTCTGACTTTTAAATGAACATTTGCTGCTTCTGCTCTCC 635
Db 558 GTATCAATTTCTGGAGAAATTTTCCAGACATTAAGATAGTATCTTTGGGGCTGTCTGCC 617
QY 636 CCTATTATTTTACATTTCTCTATGTGCAATGAGAAACACTAA-----GGTT 686
Db 618 GCTGCTTGTGATGTCATCTGCTACTCGGAATCTTGGAAATCTGCTTGGTGTGAAA 677
QY 687 CAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCGTAAATGGTAGTCTTCTTCT 746
Db 678 CGAGAGAGAGGACAGGCGTGTAGGCTTATCTTCAACCATCATGATTTGTTATTTTCT 737
QY 747 GATGTGGGCGCTTACAAATATGCAATTTTCTGTGCACTTTTCAAGAACACTTCTCCCT 806
Db 738 CTTGTGGGCTCCCTTACAAATTTGCTTCTCTGAAACACCTTCCAGGAATTTCTTTGGCCT 797
QY 807 GAGTGACTGCAAGAGCAGCTACATCTGGAAGGTTTCAACATCACTAACTCATCGC 866
Db 798 GAATAATTGACAGTCTTAAACAGTTTGAACCAAGCCATGAGGTGACAGACTCTTGG 857

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;	APPLICATION NUMBER:	US/09/023,655	
;	FILING DATE:	HEREWITH	
;	CLASSIFICATION:		
;	PRIOR APPLICATION DATA:		
;	APPLICATION NUMBER:		
;	FILING DATE:		
;	CLASSIFICATION:		
;	ATTORNEY/AGENT INFORMATION:		
;	NAME:	Zeller, Karen J.	
;	REGISTRATION NUMBER:	37,071	
;	REFERENCE/DOCKET NUMBER:	PA-0001 US	
;	TELECOMMUNICATION INFORMATION:		
;	TELEPHONE:	(650) 855-0555	
;	TELEFAX:	(650) 845-4166	
;	INFORMATION FOR SEQ ID NO:	967:	
;	SEQUENCE CHARACTERISTICS:		
;	LENGTH:	1225 base pairs	
;	TYPE:	nucleic acid	
;	STRANDEDNESS:	single	
;	TOPOLOGY:	linear	
;	IMMEDIATE SOURCE:		
;	LIBRARY:	GENBANK	
;	CLONE:	g1502408	
;	US-09-023-655-967		

Query Match	22.3%;	Score 230.6;	DB 4;	Length 1225;
Best Local Similarity	57.0%;	Pred. No. 6.6e-65;		
Matches 522;	Conservative 0;	Mismatches 354;	Indels 39;	Gaps 4;

QY	74	CAGAGCAATGTGACAAAGTATGACGCCACGAGCACTCTCAGCCACGCTGGTGCATCACTCT	133
DB	76	CGGAGCCCTGCCAAAAATCAATGTGAAGCAATCGCAGCCGCCCTCTCGCTCCGGTCT	135
QY	134	GCTCTGCTGTTTGTGATCGGTTGCTCTGGGCAATCTCTGTTTGTGCTTATCTCTGTAA	193
DB	136	ACTCACTGGTGTTCATCTTTGGTTTGTGGCAACATGCTGGTCATCTCTCATCTCTGATAA	195
QY	194	AATATAAGGACTCAAGCGGTGAAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACT	253
DB	196	ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACTGGCCATCTCTGACC	255
QY	254	TGTGTTTCTTGTCTTACCTCGCCCTTCTGGGCTCATGCTGGGGGGG-----	298
DB	256	TGTTTTTCTCTTACTGTGTCCTTCTGGGCTCACTATGTCGCCGCCAGTGGGACCTTGG	315
QY	299	---ATCCCATGTGTAATAATTCTCATTCGACTGTACTTGTGGGGCTGTACAGTGAGACAT	355
DB	316	GAATAACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCT	375
QY	356	TTTTCAATTGGCTTCTGACTGTGCAAGGTACCTAGTGTTTTTCACACAGGGCACTTTT	415
DB	376	TCCTCATCATCTCCTCGACAAATCATAGGTACCTGGCTGTCGTCCATGCTGTGTGTGCTT	435
QY	416	TCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCTCTGGCATGGGTAACAG	475
DB	436	TAAAGCC---AGGACGGTCACCTTTGGGGTGGTGACAAAGTGTGATCACTTGGGTGGTGG	492
QY	476	CCATTCTGGCCACTTTGGCTGAATTCTGTGTTTATAAACTTCAGATGGAAGACACAGAAT	535
DB	493	CTGTGTTTGGGCTCTCTCCAGGAATCATCTTTTACAGATCTCCTCAAAAAGAGGTCTTCATT	552
QY	536	ACAAGTGTGCATTTAGCAGAACTCCCTTCCGTCCAGCTGTATGACACATCTCTGGAAGCAT	595
DB	553	ACACT-----GCAGCTCTCATTTTCCATACAGTTCAGTATCAATTTCTGGAAGAAATT	603
QY	596	TTCTGACTTTAAAAATGAAATTTTCGGTTCTTGTTCCTCCCCCTATTTATTTTACATTTC	655
DB	604	TCCAGACATTAAGATAGTCACTTTGGGCTGGTCTCTGCCGCTCTCTTGTCTATGTCTATCT	663
QY	656	TCTATGTGCMAATGAGAAAAACACTA-----AGTTTCAGGAGCAGAGGTATAGCC	706
DB	664	GCTACTCGGAAATCCTTAAAACTCTGTTTCGGTTCGAAATGAGAAGAGGACACAGG	723

Db 706 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTACAGATCTCAAAAAGAGGTCTTCATT 765
Qy 536 ACAAGTGTGCAATTAGCAGAACTCCCTTCCTGCGCAGCTGATGAGACATTCCTGGAAGCAAT 595
Db 766 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTCAGTATCAAATCTCTGGAAGAATT 816
Qy 596 TTCTGACTTTAAAGATGAACATTTTCGGTCTCTGCTCCCTCCCTATTTATTTTACATTTTC 655
Db 817 TCCAGACATTAAGATAGTCATCTTGGGGCTGGTCTCCCGCTGCTTGTCTATGTCATCT 876
Qy 656 TCTATGTGCAATGAGAAAACACTA-----AGGTTGAGGAGCAGAGGTATAGCC 706
Db 877 GCTACTCGGGAATCTTAAAACTCTGCTTCGGTGTGGAATGAGAAAGAGGACAGGG 936
Qy 707 TTTTCAAGCTGTTTTGCGGTAATGAGTGTCTTCTCTGATGAGGCGCCCTACATA 766
Db 937 CTGTGAGGCTTATCTTCAACCATCATGATGTTTATTTTCTCTCTGCGCTCCCTAGACA 996
Qy 767 TTGCAATTTTCTGTCCTCACTTTCAAGAACACTTCTCCTGAGTGACTGCGAAGAGCAGCT 826
Db 997 TTGTCTCTCTGTAACACCTTCCAGGAATTTCTTTGGCTCTGAATAATTCAGTAGCTCTA 1056
Qy 827 ACAATCTGGACAAAGTGTTCACATCACTAAACTCATGCGCACCAACCACCTGCTGCATCA 886
Db 1057 ACAGTTGGACCAAGCTATGAGGTGACAGACTCTTGGATGAGCAGCTGCTGCATCA 1116
Qy 887 ACCCTCTCTGTATGCGTTCTTGATGGGACATTTAGCAAAATACCTTCGCGCTGTTTCC 946
Db 1117 ACCCATCATCTATGCTTTTGTGGGGAGAGTTTCAGAAACTACTCTTATGCTTCTTCC 1176
Qy 947 ATCTGCGTAGTAACA 961
Db 1177 AAAAGCACATTTGCCA 1191

RESULT 11

US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CRS PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: human
US-09-796-202-2

Query Match 22.3%; Score 230.6; DB 4; Length 1376;
Best Local Similarity 57.0%; Pred. No. 7.2e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
Qy 74 CAGAGCAATGCAAGTATGACGCCAGGCACTCTGAGCCAGCTGGTGCATCACTCT 133
Db 289 CGGAGCCCTGCGCAAAAATCAATGGAAGCAATGCGAGCCGCTCTCGCTCCGCTCT 348
Qy 134 GCTCTGCTGTGTGTGATCGGTCTCTGGAACAATCTCTGTTGTGCTTATCTGGTAA 193
Db 349 ACTCACTGGTTCATCTTTGGTTTGTGGCAACATGCTGTCTATCTCATCTGTATAA 408
Qy 194 AATAAAGGACTCAAGCGCTGGAAAATATCTATCTTAAACTTGGCAGTTTCTAACT 253
Db 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGCCATCTCTGACC 468
Qy 254 TGTGTTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGCG----- 298
Db 469 TGTGTTTCTTCTTACTGTGCTGCTTCTGGGCTCATGCTGCGCGCCAGTGGGACTTTG 528

Qy 299 ---ATCCATGTGTAAATTTCTCATTTGACCTGTACTTCTGCTGGGCTGTACAGTGAAGCAT 355
Db 529 GAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCT 588
Qy 356 TTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTCACAAAGGCAACTTTT 415
Db 589 TCTTCATCATCTCTCTGACAAATCATAGGTACCTGGCTGTCGTCATGCTGTGTTTGTCT 648
Qy 416 TCTCAGCAGAGGAGGCTGCTGCTGTCATCATTAACAAGTGTCTCTGTCATGCGGTAAACAG 475
Db 649 TAAAGCC---AGCAGGTCACCTTTGGGGTGTGACAAGTGTGATCACTTTGGGTGGTGG 705
Qy 476 CCATTTGCGCACCTTTGCGTGAATTCGTGTTTATAAACCTCAGATGGAAGACCAAAAT 535
Db 706 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTACAGATCTCAAAAAGAGGCTCTTCATT 765
Qy 536 ACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCAAT 595
Db 766 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTCAATTTCTGGAAGAAT 816
Qy 596 TTCTGACTTTAAATGAACATTTTCGGTTCCTGCTCCCTCTATTTATTTTACATTTTC 655
Db 817 TCCAGACATTAAGATAGTCATCTTGGGGCTGGTCTCTGCGCTGCTTGTCTCATGTCATCT 876
Qy 656 TCTATGTGCAAAATGAGAAAACACTA-----AGGTTGAGGAGCAGAGGTATAGCC 706
Db 877 GCTACTCGGGAATCTTAAAACTCTGCTTCGGTGTGGAATGAGAAAGAGGACAGGG 936
Qy 707 TTTTCAAGCTGTTTTTGGCGTAATGAGTGTCTTCTCTGATGAGGCGCCCTACATA 766
Db 937 CTGTGAGGCTTATCTTCAACCATCATGATGTTTATTTTCTCTTCTGCGCTCCCTACACA 996
Qy 767 TTGCAATTTTCTGTCCTCACTTTCAAGAACACTTCTCCTGAGTGACTGCGAAGAGCAGCT 826
Db 997 TTGTCTCTCTGTAACACCTTCCAGGAATTTCTTTGGCTCTGAATAATTCAGTAGCTCTA 1056
Qy 827 ACAATCTGGACAAAGTGTTCACATCACTAAACTCATGCGCACCAACCACCTGCTGCATCA 886
Db 1057 ACAGTTGGACCAAGCTATGCGAGTGACAGAGACTCTTGGATGAGCAGCTGCTGCATCA 1116
Qy 887 ACCCTCTCTGTATGCGTTCTTGATGGGACATTTAGCAAAATACCTTCGCGCTGTTTCC 946
Db 1117 ACCCATCATCTATGCTTTTGTGGGGAGAGTTTCAGAAACTACTCTTATGCTTCTTCC 1176
Qy 947 ATCTGCGTAGTAACA 961
Db 1177 AAAAGCACATTTGCCA 1191

RESULT 12

US-09-502-783A-1
; Sequence 1, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CRS)
; TITLE OF INVENTION: HDNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)

US-09-502-783A-1

Query Match 22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 74 CAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGGCCAGCTGTGGCCATCACTCT 133
DB 308 CGAGGCCCTGCCAAAATCAATGTGAGCAATCGAGCGCCGCTCTCGCTCGCTCT 367

QY 134 GCTCTGCTGTGTGATCGGTCTCTGCAATCTCTGGTGTGTGCTTATCTGGTAA 193
DB 368 ACTCAGTGTGTCTCTTGGTGTGTGGCAACATGCTGTGTCATCTCATCTCGTAA 427

QY 194 AATATAAGGACTCAACGCGTGGAAATATCTTCTAATCTGGCAGTCTTCAACT 253
DB 428 ACTGCAAAAGGCTGAAGAGCATGACCTGACATCTACCTGCTCAACCTGGCCATCTTGACC 487

QY 254 TGTGTTCTTGTCTTACCCCTTCTGGGCTCATGCTGGGGCG----- 298
DB 488 TGTGTTCTTGTCTTACCCCTTCTGGGCTCATGCTGGGGCGCTGCTGCTGCTGCTT 547

QY 299 ----ATCCCATGTGTAATTTCTCAATGGAATCTTCTGTTGTGCTTATCTGGTAA 355
DB 548 GAAATACAATGTGTCACCTCTTGACAGGCTCTATTTTATAGGCTTCTTCTGGAATCT 607

QY 356 TTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGCACTTTT 415
DB 608 TCTTCATCATCTCTGCAAAATCGATAGGTACCTGCTGCTGCTGCTGCTGCTGCTT 667

QY 416 TCTCAGCAGGAGGAGGCTGCTGCTGCTGCAATCAATTAAGAGTGTCTGCGCATGGTAA 475
DB 668 TAAAGGCC---AGGACGCTCACTTTGGGGTGTGACAGTGTGATCACTTTGGGTGG 724

QY 476 CCATCTGGCCACTTTGCTGTAATCTGTTGTTTATAAACCCTCAGATGGAGACAGAAAT 535
DB 725 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTTACAGATCTCAAAAGAGAGTCTTCAAT 784

QY 536 ACAGTGTGCATTTAGCAGAACTCCCTCTGCGCAGCTGATGAGACATTTCTGGAAGCAT 595
DB 785 ACACCT-----CGAGCTCTCATTTTCCATACAGTCAATATCAATTTCTGGAAGAT 835

QY 596 TCTGACTTTTAAATGAACATTTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
DB 836 TCCAGACATTAAGATAGTCACTTGGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895

QY 656 TCTATGTGCAATGAGAAACACTA-----AGGTTCAGGAGCAGAGGTATAGCC 706
DB 896 GCTACTCGGGAATCCTTAAANAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955

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DB 956 CTGTGAGGCTTATCTTCCACCATCATGATGTTTATTTTCTCTTCTGCGGCTCCCTACA 1015

QY 767 TTGCATTTTCTGCTGCTGCTTCAAGAACACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 826
DB 1016 TTGCTCTTCTGCTGCTGCTTCCAGGAATTTCTTGGCTGTAATTAATGAGTGTGCTTA 1075

QY 827 ACATCTGGAACAAGTGTTCATATCACTAACTCATCGCCACCACTGCTGCTGCTGCTGCT 886
DB 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGATGACGCACTGCTGCTGCT 1135

QY 887 ACCCTCTCTGCTGCTGCTTCTGATGGGACATTTAGCAATACCTTCTGCGCTGCTGCTTCC 946
DB 1136 ACCCATCATCTAGCTTCTGCGGGAGAGTTTCAAGAACTACCTCTTCTGCTTCTTCTTCC 1195

QY 947 ATCTGCTGTGTAACA 961
DB 1196 AAGAGCATTTGCCA 1210

RESULT 13

US-09-502-784A-1

Sequence 1, Application US/09502784A
Patent No. 6743594
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Methods of Screening Using Human G-Protein
TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
FILE REFERENCE: 1488.1150005
CURRENT APPLICATION NUMBER: US/09/502,784A
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 1
LENGTH: 1414
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (259)..(1314)
OTHER INFORMATION:
US-09-502-784A-1

Query Match 22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 74 CAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGGCCAGCTGTGGCCATCACTCT 133
DB 308 CGAGGCCCTGCCAAAATCAATGTGAGCAATCGAGCGCCGCTCTCGCTCGCTCT 367

QY 134 GCTCTGCTGTGTGATCGGTCTCTGCAATCTCTGGTGTGTGCTTATCTGGTAA 193
DB 368 ACTCAGTGTGTCTCTTGGTGTGTGGCAACATGCTGTGTCATCTCATCTCGTAA 427

QY 194 AATATAAGGACTCAACGCGTGGAAATATCTTCTAATCTGGCAGTCTTCTAACT 253
DB 428 ACTGCAAAAGGCTGAAGAGCATGACCTGACATCTACCTGCTCAACCTGGCCATCTTGACC 487

QY 254 TGTGTTCTTGTCTTACCCCTTCTGGGCTCATGCTGGGGCG----- 298
DB 488 TGTGTTCTTGTCTTACCCCTTCTGGGCTCATGCTGGGGCGCTGCTGCTGCTGCTT 547

QY 299 ----ATCCCATGTGTAATTTCTCAATGGAATCTTCTGTTGTGCTTATCTGGTAA 355
DB 548 GAAATACAATGTGTCACCTCTTGACAGGCTCTATTTTATAGGCTTCTTCTGGAATCT 607

QY 356 TTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGCACTTTT 415
DB 608 TCTTCATCATCTCTGCAAAATCGATAGGTACCTGCTGCTGCTGCTGCTGCTGCTT 667

QY 416 TCTCAGCAGGAGGAGGCTGCTGCTGCTGCAATCAATTAAGAGTGTCTGCGCATGGTAA 475
DB 668 TAAAGGCC---AGGACGCTCACTTTGGGGTGTGACAGTGTGATCACTTTGGGTGG 724

QY 476 CCATCTGGCCACTTTGCTGTAATCTGTTGTTTATAAACCCTCAGATGGAGACAGAAAT 535
DB 725 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTTACAGATCTCAAAAGAGAGTCTTCAAT 784

QY 536 ACAGTGTGCATTTAGCAGAACTCCCTCTGCGCAGCTGATGAGACATTTCTGGAAGCAT 595
DB 785 ACACCT-----CGAGCTCTCATTTTCCATACAGTCAATATCAATTTCTGGAAGAT 835

QY 596 TCTGACTTTTAAATGAACATTTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 655
DB 836 TCCAGACATTAAGATAGTCACTTGGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895

QY 656 TCTATGTGCAATGAGAAACACTA-----AGGTTCAGGAGCAGAGGTATAGCC 706
DB 896 GCTACTCGGGAATCCTTAAANAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955

QY 707 TTTTCAAGCTGTTTTTGGCGTAATGGTAGTCTTCCCTTCTGATGTGGGCGCCCTTACAATA 766
DB 956 CTGTGAGGCTTATCTTCAACCATCATGATGTTGTTATTTTCTTCTGGGCTCCCTTACAACA 1015
QY 767 TTGCATTTTCTCTGTCACATTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 826
DB 1016 TTGTGCTTCTCTGAAACACTTCCAGGAATTTCTTGGCGTGAATTAATTGCAAGTAGCTCTA 1075
QY 827 ACAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACACACCACCTGCTGCATCA 886
DB 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGATGACGCACTGCTGCATCA 1135
QY 887 ACCCTCTCTGTATGCGTTTCTGATGGGACATTTAGCAATTTAGCAATACCTCTGCGCGTGTTC 946
DB 1136 ACCCCATCATCTATGCGCTTTGTGCGGGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1195
QY 947 ATCTGCGTAGTAACA 961
DB 1196 AAAAGCACATTGCCA 1210

RESULT 14

US-09-339-912A-1
; Sequence 1, Application US/09339912A
; Patent No. 6759519
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-339-912A-1

Query Match 22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 74 CAGAGCAATGTGACAGTAGACGCCAGGCACTCTCAGGCCAGCTGGTGCATCATCT 133
DB 308 CGGAGCCCTCGCAAAAATCAATGTGAAGCAATCGCAGCCGCTCTCGCTCGCTCT 367
QY 134 GCTCTGCTGTGTTGTGATCGGTCTCTGACATCTCTCGGTGTGCTTATCTGTGTA 193
DB 368 ACTCAGTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGTGTCATCTCATCTGAT 427
QY 194 AATAAAGGACTCAAGCGTGGAAATATCTATCTTAACTGCGAGTTTCTAACT 253
DB 428 ACTGCAAAAGGCTGGAAGCATGACTGACATCTACTGCTCTCAACTGGCCATCTTGACC 487
QY 254 TGTGTTTCTTGTACCTGCGCTTCTGGGCTCATGCTGGGGCG----- 298
DB 488 TGTGTTTCTTGTACTGTCCCTTCTGGGCTCACTATGCTGCGCCAGGAGGACTTTG 547
QY 299 ----ATCCCATGTGAAAATTTCTATGACATGTAATCTGCTGGGCTGTACAGTACAT 355
DB 548 GAAATACAAATGTGCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGAAATCT 607

QY 356 TTTTCAATGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCACAAGGGCAACTTTT 415
DB 608 TCTTCATCATCTCTCTGACAAATCGATAGGTACCTGGCTGTCTGCATGCTGTGTTGCTT 667
QY 416 TCTCAGCAGGAGGAGGCTGCTGGGCATCATTAACAAGTGTCTGGCATGGGTAAACAG 475
DB 668 TAAAGCC----AGACCGTCACTTTGGGGTGGTGAACAGTGTGATCACTTGGGTGGTGG 724
QY 476 CCATTTCTGGCCACTTTGCTCGAATTCGTGGTTTATAAACCTCAGATGGAAGACAGAAAT 535
DB 725 CTGTGTTGGGTCTCTCCCAAGGAATCATCTTACCAGATCTCAAAAAGGAAGGTCTTCATT 784
QY 536 ACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAAT 595
DB 785 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAT 835
QY 596 TTCTGACTTTAAAAATGAACATTTCCGTTTCTGCTCCCTCCCTATTTATTTTACATTTT 655
DB 836 TCCAGACATTTAAAGATAGTCACTTTGGGGCTGGTCTGCGCGCTGCTTGTCAATGTCATCT 895
QY 656 TCTATGTGCAATGAGAAACACTA-----AGTTTCAGGGAGCAGAGGTATAGCC 706
DB 896 GCTACTCGGAATCTTAAAACTCTGCTTCGGTGTGAAATGAGAAGAGGACAGGG 955
QY 707 TTTTCAAGCTGTTTTTGGCGTAATGGTAGTCTTCTTCTGATGTGGGCGCCCTTACAATA 766
DB 956 CTGTGAGGCTTATCTTCAACCATCATGATTTTATTTTCTTCTCTGCGGCTCCCTTACAACA 1015
QY 767 TTGCATTTTCTGCTCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 826
DB 1016 TTGTCTTCTCTGGAACACTTCCAGGAATTTCTTGGCGCTGAAATTAATTGCAAGTAGCTCTA 1075
QY 827 ACAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACCCACCCTGCTGCATCA 886
DB 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGATGACGCACTGCTGCATCA 1135
QY 887 ACCCTCTCTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGCGTGTTC 946
DB 1136 ACCCATCATCTATGCTTGTGCGGGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1195
QY 947 ATCTGCGTAGTAACA 961
DB 1196 AAAAGCACATTGCCA 1210

RESULT 15

US-09-195-662A-1
; Sequence 1, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-195-662A-1

Query Match 22.3%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 7.3e-65;

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Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
Qy 74 CAGGCAATGTGCAAGTATGAGCCAGGCACTCTCAGCCAGCTGGTGGCACTCACTCT 133
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Qy 308 CGGAGCCCTGCCAAAATCAATGTGAAGCAAAATCGCAGCCGCCCTCTCCCTCCGCTCT 367
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Qy 134 GCTCTGCTGTGTTTGTGATCGGTCTCTCGACAAATCTCTGGTGTGCTTATCTCGTAA 193
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Qy 368 ACTCACTGTGTTCATCTTTGGTTTGTGGCAACATGCTGGTCACTCTCTGATAA 427
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 194 AATATAAGGACTCAAAACGGTGAATAATCTATCTTAAACTTTGGCAGTTTCTAACT 253
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 428 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGTCAACCTGGCCATCTCTGACC 487
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 254 TGTGTTTCTTGTCTTACCTGCCCTCTGGGCTCATGCTGGGGG----- 298
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 488 TGTGTTTCTTGTCTTACCTGCCCTCTGGGCTCACTATGCTGGCCGACGTGGGACTTTG 547
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 299 ---ATCCCATGTGTAAAATTTCTCATTTGAGCTGTACTTCGTGGGCTGTACAGTGAGACAT 355
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 548 GAAATACATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTTGGATCT 607
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 356 TTTTCAATGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTGGCAAGGGCAACTTTT 415
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 608 TCTTCATCATCTCTGACAAATCGATAGGTACCTGGCTGCTGCCATGCTGTGTTGCTT 667
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416 TCTCAGCCAGGAGGGTGGCTCTGGCATCATACAGTGTCTTGGCATGGTAAACAG 475
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Qy 668 TAAAGGCC---AGGACGGTCACCTTTGGGGTGGTGAAGTGTGATCACTTGGGTGGTGG 724
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 476 CCATTTCTGGCCACTTTTGCCTGAATTCGTGGTGTATTAACCTCAGATGGAAGACAGAAAT 535
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Qy 725 CTGTGTTGGGTCTCTCCAGGATCATCTTTACCAGATCTCAAAAAGAGGTCTTCATT 784
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Qy 536 ACAAGTGTGATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATTTGGAAGCAT 595
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 785 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 835
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 596 TTCTGACTTTAAAATGAACATTTGGTTCCTGCTCCCTCCCTATTTATTTTACATTTC 655
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Qy 836 TCCAGACATTAAGATAGTATCTTTGGGGTGGTCTGCGCTGCTTGTGTCATGGTCACT 895
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Qy 656 TCTATGTGCAAAATGAGAAAACACTA-----AGGTTTCAGGGAGCAGAGGTATAGCC 706
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 896 GCTACTCGGGAATCCTAAAACCTGTCTCGGTGCGAAATGAGAAGAGGCAAGGG 955
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 707 TTTTCAAGCTGTTTTCGCGTAATGTAGTCTTCTTCTGATGTGGGGCCCTACAATA 766
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 956 CTGTGAGGCTTATCTTCAACCATCATGATTTGTTATTTTCTTCTGGGCTCCCTACAACA 1015
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 767 TTGCATTTTTCCTGTCCACTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 826
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1016 TTGTCCTTCTCCGAAACACCTTCAGGAATTTCTTTGGCCTGAATAATTCAGTAGTCTTA 1075
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Qy 827 ACAATCTGGAACAAAGTGTTCACATCACTAAACTCATGCGCCACCCACTGCTGCATCA 886
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Qy 1076 ACAGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGGATGACCGCACTGCTGCATCA 1135
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Qy 887 ACCCTCTCTGTATGCGTTTCTTGAAGGACATTTAGCAAAATACCTCTGCCGCTGTTTC 946
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Qy 1136 ACCCATCATCTATGCTTTGTCGGGGAGAAGTTTCAGAACTACCTCTTAGTCTTCTTCC 1195
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 947 ATCTGCGTAGTAACA 961
Db ||||| ||||| |||||
Qy 1196 AAAAGCACATTGGCA 1210
Db ||||| ||||| |||||
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Search completed: June 18, 2005, 12:14:47
Job time : 203.888 secs


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QY 181 CTTATCTCGTAAATATATAAGGACTCAACCGCGTGGAAATATATCTATCTCTAAACTTG 240
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QY 241 GCAGTTTCTAACTGCTGTTCTTCTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGCCAT 300
Db 325 GCAGTTTCTAACTGCTGTTCTTCTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGCCAT 384
QY 301 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTATGAGTGAGACATTTTTTC 360
Db 385 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTATGAGTGAGACATTTTTTC 444
QY 361 AATGCTCTTGTAGTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 420
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QY 421 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAACGCCATT 480
Db 505 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAACGCCATT 564
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QY 541 TGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGAGCAATTTCTG 600
Db 625 TGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGAGCAATTTCTG 684
QY 601 ACTTTAAATAATGAACATTTCCGTTCTTCTGCTCCCTTATTTATTTTACATTTCTCTAT 660
Db 685 ACTTTAAATAATGAACATTTCCGTTCTTCTGCTCCCTTATTTATTTTACATTTCTCTAT 744
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QY 781 TCCACTTTCAAGAACACTTCTCCCTGAGTGCAGTGCAGAGCAGCTACAATCTGACAAA 840
Db 924 TCCACTTTCAAGAACACTTCTCCCTGAGTGCAGTGCAGAGCAGCTACAATCTGACAAA 984
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QY 1021 TCCACCGAAGTGTAA 1035
Db 1105 TCCACCGAAGTGTAA 1119
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RESULT 3
US-10-754-071-11
; Sequence 11, Application US/10754071
; Publication No: US20040137578A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Chemokine TECK Polypeptides
; FILE REFERENCE: DX0589K1C US

; CURRENT APPLICATION NUMBER: US/10/754,071
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 10/039,659
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-754-071-11

Query Match 100.0%; Score 1035; DB 19; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCCCAATTACACGCTGGCACAGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
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QY 61 GAGAGCGATGAGGAGCAGCAATGTGACAAAGTATGACGCCCGCAGGCACTCTCAGCCAGCTG 120
Db 145 GAGAGCGATGAGGAGCAGCAATGTGACAAAGTATGACGCCCGCAGGCACTCTCAGCCAGCTG 204
QY 121 GTGCCATCACTCTCTCTGCTGTTGTGATCGGTTGCTGCGGATGCTGAGCAATCTCTCTGTTGTG 180
Db 205 GTGCCATCACTCTCTCTGCTGTTGTGATCGGTTGCTGCGGATGCTGAGCAATCTCTCTGTTGTG 264
QY 181 CTTATCTCGTAAATATATAAGGACTCAACCGCGTGGAAATATCTATCTCTAAACTTG 240
Db 265 CTTATCTCGTAAATATATAAGGACTCAACCGCGTGGAAATATCTATCTCTAAACTTG 324
QY 241 GCAGTTTCTAACTGCTGTTCTTCTTACCCTGCTTCTGGGCTCATGCTGGGGCCAT 300
Db 325 GCAGTTTCTAACTGCTGTTCTTCTTACCCTGCTTCTGGGCTCATGCTGGGGCCAT 384
QY 301 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTTC 360
Db 385 CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCTGTACAGTGAGACATTTTTTC 444
QY 361 AATGCTCTTGTAGTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 420
Db 445 AATGCTCTTGTAGTGTGCAAGGTACCTAGTGTGTTTTTGGCAAGGGCAACTTTTTCTCA 504
QY 421 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAACGCCATT 480
Db 505 GCCAGGAGGGTCCCTGTGGCATCAATCAAGTGTCTGGCATGGTAACGCCATT 564
QY 481 CTGGCCACTTTGCCCTGAATTCGTGGTGTATTAACCTCAGATGGAAGACCAAGATACAA 540
Db 565 CTGGCCACTTTGCCCTGAATTCGTGGTGTATTAACCTCAGATGGAAGACCAAGATACAA 624
QY 541 TGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGAGCAATTTCTG 600
Db 625 TGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGAGCAATTTCTG 684
QY 601 ACTTTAAATAATGAACATTTCCGTTCTTCTGCTCCCTTATTTATTTTACATTTCTCTAT 660
Db 685 ACTTTAAATAATGAACATTTCCGTTCTTCTGCTCCCTTATTTATTTTACATTTCTCTAT 744
QY 661 GTGCAATGAGAAAAACAATAAGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
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Db 745 GTGCAATGAGAAAAACACTAAGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 804
Qy 721 TTTGGCGTAATGTAGTCTTCTCTGATGTGGGCGCCCTACAAATATGCAATTTTCCCTG 780
Db 805 TTTGGCGTAATGTAGTCTTCTCTGATGTGGGCGCCCTACAAATATGCAATTTTCCCTG 864
Qy 781 TCCACTTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 840
Db 865 TCCACTTTTCAAGAAACACTTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 924
Qy 841 AGTGTTCACATCACTAACTCATCGCCACCAACCCTGCTGCATCAACCCCTCTCTGTAT 900
Db 925 AGTGTTCACATCACTAACTCATCGCCACCAACCCTGCTGCATCAACCCCTCTCTGTAT 984
Qy 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCATCTGCGTAGTAAC 960
Db 985 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCATCTGCGTAGTAAC 1044
Qy 961 ACCCCACTTCAACCCAGGGGGAGTCTGCACAAAGGCACATCGAGGGAAAGAACCTGACCAT 1020
Db 1045 ACCCCACTTCAACCCAGGGGGAGTCTGCACAAAGGCACATCGAGGGAAAGAACCTGACCAT 1104
Qy 1021 TCCACCGAAGTGTA 1035
Db 1105 TCCACCGAAGTGTA 1119

RESULT 4

US-10-759-860-11
; Sequence 11, Application US/10759860
; Publication No. US20050074790A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for using chemokine TECK
; FILE REFERENCE: DX0589KID US
; CURRENT APPLICATION NUMBER: US/10/759,860
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 10/039,659
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-759-860-11

Query Match 100.0%; Score 1035; DB 21; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCCAATTACAGCTGGCCACAGAGGATGAATATGATCTCTCATAGAGGTGAAGT 60
Db 85 ATGCCCAATTACAGCTGGCCACAGAGGATGAATATGATCTCTCATAGAGGTGAAGT 144
Qy 61 GAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCCGAGGCACTCTCAGCCGAGCTG 120

RESULT 5

US-10-741-600-12
; Sequence 12, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:

Db 145 GAGAGCGATGAGGAGAGCAATGTGCAAGTATAGCGCCAGGCACTCTCAGCCGAGCTG 204
Qy 121 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGCTCTGGACAATCTCTCTGGTGTG 180
Db 205 GTGCCATCACTCTGCTCTGCTGTTGTGATCGGTGCTCTGGACAATCTCTCTGGTGTG 264
Qy 181 CTTATCTCTGTAATAATATAAGGACTCAAAACGCGTGGAAAAATATCTATCTTTAAACTTG 240
Db 265 CTTATCTCTGTAATAATATAAGGACTCAAAACGCGTGGAAAAATATCTATCTTTAAACTTG 324
Qy 241 GCAGTTTCTAACTTGTGTTTCTGTTTACCTGCTCCCTCTGCGGCTCATGCTGGGGCGAT 300
Db 325 GCAGTTTCTAACTTGTGTTTCTGTTTACCTGCTCCCTCTGCGGCTCATGCTGGGGCGAT 384
Qy 301 CCCATGTGTAATAATCTCATTTGGACTGACTTCTGCTGGGCTGTACAGTGAGACATTTTTC 360
Db 385 CCCATGTGTAATAATCTCATTTGGACTGACTTCTGCTGGGCTGTACAGTGAGACATTTTTC 444
Qy 361 AATTGCTTCTGACTGTGCAAGAGTACCTAGTGTGTTTTTGCACAAGGGCAACTTTTCTCA 420
Db 445 AATTGCTTCTGACTGTGCAAGAGTACCTAGTGTGTTTTTGCACAAGGGCAACTTTTCTCA 504
Qy 421 GCAGAGGAGGCTGCTGCTGTCATTAACAAGTCTCTGSCATGGGTAAACAGCAATT 480
Db 505 GCAGAGGAGGCTGCTGCTGTCATTAACAAGTCTCTGSCATGGGTAAACAGCAATT 564
Qy 481 CTGGCCACTTTCCTGAATTCGTGGTTTATAAACCTCAGATGGAACACAGAAATACAAG 540
Db 565 CTGGCCACTTTCCTGAATTCGTGGTTTATAAACCTCAGATGGAACACAGAAATACAAG 624
Qy 541 TGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAATTTCTG 600
Db 625 TGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAATTTCTG 684
Qy 601 ACTTTAAAAATGAAACATTTGCTGCTCCCTCTATTTATTTTACATTTCTCTAT 660
Db 685 ACTTTAAAAATGAAACATTTGCTGCTCCCTCTATTTATTTTACATTTCTCTAT 744
Qy 661 GTGCAATGAGAAACACTAAGGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db 745 GTGCAATGAGAAACACTAAGGTTTCAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 804
Qy 721 TTTGCGGTAAATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCATTTTCCCTG 780
Db 805 TTTGCGGTAAATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCATTTTCCCTG 864
Qy 781 TCACATTTCAAAGAAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 840
Db 865 TCACATTTCAAAGAAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAAATCTGGACAA 924
Qy 841 AGTGTTCACATCACTAACTCATCGCCACCAACCCTGCTGCAATCAACCTCTCTGTAT 900
Db 925 AGTGTTCACATCACTAACTCATCGCCACCAACCCTGCTGCAATCAACCTCTCTGTAT 984
Qy 901 GCGTTTCTTGTGGGACATTTAGCAATATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC 960
Db 985 GCGTTTCTTGTGGGACATTTAGCAATATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC 1044
Qy 961 ACCCCACTTCAACCCAGGGGGAGTCTGCACAAAGGCACATCGAGGGAAAGAACCTGACCAT 1020
Db 1045 ACCCCACTTCAACCCAGGGGGAGTCTGCACAAAGGCACATCGAGGGAAAGAACCTGACCAT 1104
Qy 1021 TCCACCGAAGTGTA 1035
Db 1105 TCCACCGAAGTGTA 1119

QY	721	TTTGCCGTAATGAGTGTCTTCTTCTGATGTGGGCGCCCTCAATAATTTGCAATTTTCTCTG	780
DB	733	TTTGCCGTAATGAGTGTCTTCTTCTGATGTGGGCGCCCTCAATAATTTGCAATTTTCTCTG	792
QY	781	TCCACTTTTCAAGAACACATTTCTCCCTGAGTGTGCAAGAGCAGCTACAACTCTGGACAAA	840
DB	793	TCCACTTTTCAAGAACACATTTCTCCCTGAGTGTGCAAGAGCAGCTACAACTCTGGACAAA	852
QY	841	AGTGTTCACATCACTAAATCTCATCGCCACACCCACTGTGTCATCAACCCCTCTCTCTGTAT	900
DB	853	AGTGTTCACATCACTAAATCTCATCGCCACACCCACTGTGTCATCAACCCCTCTCTCTGTAT	912
QY	901	GGTGTTCATGAGGACATTTAGCAAAATACCTCTGCGCTGTTTTCATCTGCGTAGTAAC	960
DB	913	GGTGTTCATGAGGACATTTAGCAAAATACCTCTGCGCTGTTTTCATCTGCGTAGTAAC	972
QY	961	ACCCCACTTCAACCCAGGGGAGTGTGCACAGGACACATCGAGGGAAGAACCTGACCAT	1020
DB	973	ACCCCACTTCAACCCAGGGGAGTGTGCACAGGACACATCGAGGGAAGAACCTGACCAT	1032
QY	1021	TCCACCGAAGTGTAA	1035
DB	1033	TCCACCGAAGTGTAA	1047
RESULT 9			
US-10-223-085-15			
; Sequence 15, Application US/10223085			
; Publication No. US20030100497A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Ferrera, Napoleone			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Marsters, Scot A.			
; APPLICANT: Pan, James			
; APPLICANT: Stephan, Jean-Philippe F.			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Ye, Weilan			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS			
; FILE REFERENCE: P3235PIC10			
; CURRENT APPLICATION NUMBER: US/10/223,085			
; CURRENT FILING DATE: 2002-08-16			
; PRIOR APPLICATION NUMBER: US 10/081,056			
; PRIOR FILING DATE: 2002-02-20			
; PRIOR APPLICATION NUMBER: US 60/213,637			
; PRIOR FILING DATE: 2000-06-23			
; PRIOR APPLICATION NUMBER: US 60/219,556			
; PRIOR FILING DATE: 2000-07-20			
; PRIOR APPLICATION NUMBER: US 60/220,624			
; PRIOR FILING DATE: 2000-07-25			
; PRIOR APPLICATION NUMBER: US 60/220,664			
; PRIOR FILING DATE: 2000-07-25			
; PRIOR APPLICATION NUMBER: PCT/US00/20710			
; PRIOR FILING DATE: 2000-07-28			
; PRIOR APPLICATION NUMBER: US 60/222,695			
; PRIOR FILING DATE: 2000-08-02			
; PRIOR APPLICATION NUMBER: US 09/643,657			
; PRIOR FILING DATE: 2000-08-17			
; PRIOR APPLICATION NUMBER: PCT/US00/23522			
; PRIOR FILING DATE: 2000-08-23			
; PRIOR APPLICATION NUMBER: PCT/US00/23328			
; PRIOR FILING DATE: 2000-08-24			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 383			

; SEQ ID NO 15									
; LENGTH: 1475									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-223-085-15									
Query Match 99.7%; Score 1031.8; DB 15; Length 1475;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGCGCAATTACACGCTGGCACCAGAGGATGAATATGATCTCTCATAGAGGTGAAC	60						
DB	29	ATGCGCAATTACACGCTGGCACCAGAGGATGAATATGATCTCTCATAGAGGTGAAC	88						
QY	61	GAGAGCGATGAGGAGAGCAATGTGACAAATATGAGCCCGAGGCACTCTCAGCCGAG	120						
DB	89	GAGAGCGATGAGGAGAGCAATGTGACAAATATGAGCCCGAGGCACTCTCAGCCGAG	148						
QY	121	GTGCCATCACTGCTGCTGCTGTTGTGATCGGTGCTGCGACAAATCTCCTGGTTG	180						
DB	149	GTGCCATCACTGCTGCTGCTGTTGTGATCGGTGCTGCGACAAATCTCCTGGTTG	208						
QY	181	CTTATCTCGTAAATATAAGGACTCAACGCGGTGGAAATATCTATCTTCTAAACT	240						
DB	209	CTTATCTCGTAAATATAAGGACTCAACGCGGTGGAAATATCTATCTTCTAAACT	268						
QY	241	GCAGTTTCTAATCTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	300						
DB	269	GCAGTTTCTAATCTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	328						
QY	301	CCATGTGTAATATCTCATTTGACGTGACTCTGTTGGGCTGTACAGTGAGACATTT	360						
DB	329	CCATGTGTAATATCTCATTTGACGTGACTCTGTTGGGCTGTACAGTGAGACATTT	388						
QY	361	AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCACTTTTCT	420						
DB	389	AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCACTTTTCT	448						
QY	421	GCAGAGGAGGGTGCCTGTGGATCATTAAGTGTCTGGGATGGGTAAACAGCCAT	480						
DB	449	GCAGAGGAGGGTGCCTGTGGATCATTAAGTGTCTGGGATGGGTAAACAGCCAT	508						
QY	481	CTGSCCACTTTGCTGAATTCGTGTTTATAAACCCTCAGATGAAGACCAAGAAAT	540						
DB	509	CTGSCCACTTTGCTGAATTCGTGTTTATAAACCCTCAGATGAAGACCAAGAAAT	568						
QY	541	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCA	600						
DB	569	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCA	628						
QY	601	ACTTTAAATATGAACATTTTCGGTTCTGTCTCCCTCTATTTATTTTACATTTCT	660						
DB	629	ACTTTAAATATGAACATTTTCGGTTCTGTCTCCCTCTATTTATTTTACATTTCT	688						
QY	661	GTCAATATGAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCCTTTCAAGCT	720						
DB	689	GTCAATATGAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCCTTTCAAGCT	748						
QY	721	TTTGGCCGATAGTGTGTTCTTCTTCTGATGTGGGCGCTTACAAATATTTGCA	780						
DB	749	TTTGGCCGATAGTGTGTTCTTCTTCTGATGTGGGCGCTTACAAATATTTGCA	808						
QY	781	TCACATTTCAAAGAACATTTCTCCCTGAGTGACTGCAAGAGAGCTTACAAATCT	840						
DB	809	TCACATTTCAAAGAACATTTCTCCCTGAGTGACTGCAAGAGAGCTTACAAATCT	868						
QY	841	AGTGTTCACATCACTAACTCATCGCCACCACTGCTGTCATCAACCTCTCTCT	900						
DB	869	AGTGTTCACATCACTAACTCATCGCCACCACTGCTGTCATCAACCTCTCTCT	928						
QY	901	GCGTTCCTGATGGGACATTTAGCAATATCTCTGCGGCTGTTTCCATCTCGGT	960						
DB	929	GCGTTCCTGATGGGACATTTAGCAATATCTCTGCGGCTGTTTCCATCTCGGT	988						
; SEQ ID NO 15									
; LENGTH: 1475									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-223-084-15									
Query Match 99.7%; Score 1031.8; DB 15; Length 1475;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	ATGCGCAATTACACGCTGGCACCAGAGGATGAATATGATCTCTCATAGAGGTGAAC	60						
DB	29	ATGCGCAATTACACGCTGGCACCAGAGGATGAATATGATCTCTCATAGAGGTGAAC	88						
QY	61	GAGAGCGATGAGGAGAGCAATGTGACAAATATGAGCCCGAGGCACTCTCAGCCGAG	120						
DB	89	GAGAGCGATGAGGAGAGCAATGTGACAAATATGAGCCCGAGGCACTCTCAGCCGAG	148						
QY	121	GTGCCATCACTGCTGCTGCTGTTGTGATCGGTGCTGCGACAAATCTCCTGGTTG	180						
DB	149	GTGCCATCACTGCTGCTGCTGTTGTGATCGGTGCTGCGACAAATCTCCTGGTTG	208						
QY	181	CTTATCTCGTAAATATAAGGACTCAACGCGGTGGAAATATCTATCTTCTAAACT	240						
DB	209	CTTATCTCGTAAATATAAGGACTCAACGCGGTGGAAATATCTATCTTCTAAACT	268						
QY	241	GCAGTTTCTAATCTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	300						
DB	269	GCAGTTTCTAATCTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTGGGGCGAT	328						
QY	301	CCATGTGTAATATCTCATTTGACGTGACTCTGTTGGGCTGTACAGTGAGACATTT	360						
DB	329	CCATGTGTAATATCTCATTTGACGTGACTCTGTTGGGCTGTACAGTGAGACATTT	388						
QY	361	AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCACTTTTCT	420						
DB	389	AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCACTTTTCT	448						
QY	421	GCAGAGGAGGGTGCCTGTGGATCATTAAGTGTCTGGGATGGGTAAACAGCCAT	480						
DB	449	GCAGAGGAGGGTGCCTGTGGATCATTAAGTGTCTGGGATGGGTAAACAGCCAT	508						
QY	481	CTGSCCACTTTGCTGAATTCGTGTTTATAAACCCTCAGATGAAGACCAAGAAAT	540						
DB	509	CTGSCCACTTTGCTGAATTCGTGTTTATAAACCCTCAGATGAAGACCAAGAAAT	568						
QY	541	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCA	600						
DB	569	TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCA	628						
QY	601	ACTTTAAATATGAACATTTTCGGTTCTGTCTCCCTCTATTTATTTTACATTTCT	660						
DB	629	ACTTTAAATATGAACATTTTCGGTTCTGTCTCCCTCTATTTATTTTACATTTCT	688						
QY	661	GTCAATATGAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCCTTTCAAGCT	720						
DB	689	GTCAATATGAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCCTTTCAAGCT	748						
QY	721	TTTGGCCGATAGTGTGTTCTTCTTCTGATGTGGGCGCTTACAAATATTTGCA	780						
DB	749	TTTGGCCGATAGTGTGTTCTTCTTCTGATGTGGGCGCTTACAAATATTTGCA	808						
QY	781	TCACATTTCAAAGAACATTTCTCCCTGAGTGACTGCAAGAGAGCTTACAAATCT	840						
DB	809	TCACATTTCAAAGAACATTTCTCCCTGAGTGACTGCAAGAGAGCTTACAAATCT	868						
QY	841	AGTGTTCACATCACTAACTCATCGCCACCACTGCTGTCATCAACCTCTCTCT	900						
DB	869	AGTGTTCACATCACTAACTCATCGCCACCACTGCTGTCATCAACCTCTCTCT	928						
QY	901	GCGTTCCTGATGGGACATTTAGCAATATCTCTGCGGCTGTTTCCATCTCGGT	960						
DB	929	GCGTTCCTGATGGGACATTTAGCAATATCTCTGCGGCTGTTTCCATCTCGGT	988						


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Db 89 GAGAGCGATAGGCGAGCAAGATGTGAAGAATGACGCCCGAGGCACTCTCAGCCAGCTG 148
Qy 121 GTGCCATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 149 GTGCCATCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
Qy 181 CTTATCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTTCTAAACTTG 240
Db 209 CTTATCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTTCTAAACTTG 268
Qy 241 GCAGTTTCTAACTTGTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 269 GCAGTTTCTAACTTGTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
Qy 301 CCCATGTGTTAAATTTCTCATTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 329 CCCATGTGTTAAATTTCTCATTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 388
Qy 361 AATTGCTTCTGAGTGTGCAAAAGTACTAGTGTGTTTGGCAAAAGGCACTTTTCTCA 420
Db 389 AATTGCTTCTGAGTGTGCAAAAGTACTAGTGTGTTTGGCAAAAGGCACTTTTCTCA 448
Qy 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 449 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508
Qy 481 CTGCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 509 CTGCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
Qy 541 TGTGCACTTTAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 569 TGTGCACTTTAGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 628
Qy 601 ACTTTAAATAGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 629 ACTTTAAATAGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 688
Qy 661 GTGCAATGAGAAAACACTAAGGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db 689 GTGCAATGAGAAAACACTAAGGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 748
Qy 721 TTTGCCGTAATGTTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 749 TTTGCCGTAATGTTAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
Qy 781 TCCACTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAA 840
Db 809 TCCACTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAA 868
Qy 841 AGTGTTCAACATCACTAAACTCATGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 869 AGTGTTCAACATCACTAAACTCATGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
Qy 901 GCGTTTCTGATGGGACATTTAGCAATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 929 GCGTTTCTGATGGGACATTTAGCAATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
Qy 961 ACCCACTTCAACCCAGGGGAGCTGCTGCAAGGCACTGAGGGAAGAACCTGACCAT 1020
Db 989 ACCCACTTCAACCCAGGGGAGCTGCTGCAAGGCACTGAGGGAAGAACCTGACCAT 1048
Qy 1021 TCCACCGAAGTGTA 1035
Db 1049 TCCACCGAAGTGTA 1063
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RESULT 11

US-10-223-088-15

; Sequence 15, Application US/10223088

; Publication No. US20030105012A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

```
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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; FILE REFERENCE: P3235P1C6
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; CURRENT APPLICATION NUMBER: US/10/223,088
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; CURRENT FILING DATE: 2002-08-16
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; PRIOR APPLICATION NUMBER: US 10/081,056
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; PRIOR FILING DATE: 2002-02-20
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; PRIOR APPLICATION NUMBER: US 60/213,637
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; PRIOR FILING DATE: 2000-06-23
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; PRIOR APPLICATION NUMBER: US 60/219,556
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; PRIOR FILING DATE: 2000-07-20
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; PRIOR APPLICATION NUMBER: US 60/220,624
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; PRIOR FILING DATE: 2000-07-25
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; PRIOR APPLICATION NUMBER: US 60/220,664
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; PRIOR FILING DATE: 2000-07-25
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; PRIOR APPLICATION NUMBER: PCT/US00/20710
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; PRIOR FILING DATE: 2000-07-28
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; PRIOR APPLICATION NUMBER: US 60/222,695
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; PRIOR FILING DATE: 2000-08-02
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; PRIOR APPLICATION NUMBER: US 09/643,657
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; PRIOR FILING DATE: 2000-08-17
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; PRIOR APPLICATION NUMBER: PCT/US00/23522
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; PRIOR FILING DATE: 2000-08-23
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR FILING DATE: 2000-08-24
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; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 383
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; SEQ ID NO 15
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; LENGTH: 1475
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; TYPE: DNA
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; ORGANISM: Homo sapiens
```

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; US-10-223-088-15
```

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Query Match 99.7%; Score 1031.8; DB 15; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCAATTACAGCTGGCCAGGAGGATGAATATGATGTCCTCATAGAGGTGAAGCTG 60
Db 29 ATGCCCAATTACAGCTGGCCAGGAGGATGAATATGATGTCCTCATAGAGGTGAAGCTG 88
Qy 61 GAGAGCGATGAGGAGGAGCAATGTGAAGTATGACGCCCGAGGCACTCTCAGCCAGCTG 120
Db 89 GAGAGCGATGAGGAGGAGCAATGTGAAGTATGACGCCCGAGGCACTCTCAGCCAGCTG 148
Qy 121 GTGCCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 149 GTGCCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
Qy 181 CTTATCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTTCTAAACTTG 240
Db 209 CTTATCTGTTAAATATAAAGGACTCAAGCGCTGGAAATATCTATCTTCTAAACTTG 268
Qy 241 GCAGTTTCTAACTTGTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 269 GCAGTTTCTAACTTGTGTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
Qy 301 CCATGTGTTAAATTTCTCATTTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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Db 329 CCGATGTGTAATAATCTCATTTGGACTGTACTTCTGGGGCTGTACAGTGAGACATTTTTC 388
Qy 361 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTTTTGCAAGGGCACTTTTCTCA 420
Db 389 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTTTTGCAAGGGCACTTTTCTCA 448
Qy 421 GCCAGAGGAGGGTGCCTCTGGCATCATTAACAAGTGTCTCTGGCATGGGTAACAGCCATT 480
Db 449 GCCAGAGGAGGGTGCCTCTGGCATCATTAACAAGTGTCTCTGGCATGGGTAACAGCCATT 508
Qy 481 CTGGCCACTTTGGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG 540
Db 509 CTGGCCACTTTGGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG 568
Qy 541 TGTGCATTTAGCAGAACTCCCTCTCCGCACTGTAGACATTCGGAAGCAATTTCTG 600
Db 569 TGTGCATTTAGCAGAACTCCCTCTCCGCACTGTAGACATTCGGAAGCAATTTCTG 628
Qy 601 ACTTTAAAAATGAACATTTCCGGTCTTGTCTCCCTCCCTATTTATTTTACATTTCTCTAT 660
Db 629 ACTTTAAAAATGAACATTTCCGGTCTTGTCTCCCTCCCTATTTATTTTACATTTCTCTAT 688
Qy 661 GTCAAAATGAAAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT 720
Db 689 GTCAAAATGAAAAACACATTAAGTTTCAGGAGCAGAGGTATAGCCCTTTTCAAGCTTGT 748
Qy 721 TTTGCCGTATGTAGTCTTCTCTGATGTGGGGCCCTACAAATTTGCAATTTTCCCTG 780
Db 749 TTTGCCATAATGTAGTCTTCTCTGATGTGGGGCCCTACAAATTTGCAATTTTCCCTG 808
Qy 781 TCCACTTTCAAAGAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACAACTCTGGACAA 840
Db 809 TCCACTTTCAAAGAACACTTCTCCCTGAGTACTGCAAGAGCAGCTACAACTCTGGACAA 868
Qy 841 AGTGTTCACATCACTAACTCATCGCCACCAACCCTGTGTCATCAACCCCTCTCTGTAT 900
Db 869 AGTGTTCACATCACTAACTCATCGCCACCAACCCTGTGTCATCAACCCCTCTCTGTAT 928
Qy 901 GCCTTTCTTATGGGACATTTAGCAATACCTCTGGCGCTGTTTCCATCTGCGTAGTAAC 960
Db 929 GCCTTTCTTATGGGACATTTAGCAATACCTCTGGCGCTGTTTCCATCTGCGTAGTAAC 988
Qy 961 ACCCCACTTCAACCCAGGGGGCAGTCTGCACAAAGGCACATCGAGGGAAGAACTTGACCAT 1020
Db 989 ACCCCACTTCAACCCAGGGGGCAGTCTGCACAAAGGCACATCGAGGGAAGAACTTGACCAT 1048
Qy 1021 TCCACCGAAGTGAA 1035
Db 1049 TCCACCGAAGTGAA 1063

RESULT 12
US-10-223-090-15
; Sequence 15, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

; FILE REFERENCE: P3235P1C2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-090-15

Query Match 99.7%; Score 1031.8; DB 15; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCTCATAGAAGTGAACGTG 60
Db 29 ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCTCATAGAAGTGAACGTG 88
Qy 61 GAGAGCGATGAGCAGAGCAATGTGACAGTATGAGCCCGAGCCTCTCAGCCAGCTG 120
Db 89 GAGAGCGATGAGCAGAGCAATGTGACAGTATGAGCCCGAGCCTCTCAGCCAGCTG 148
Qy 121 GTGCCATCACTCTGCTCTGCTG 180
Db 149 GTGCCATCACTCTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 208
Qy 181 CTTATCCTCGTAAATATATAAGGACTCAAAACGCGTGGAAATATCTATCTTTTAAACTTG 240
Db 209 CTTATCCTCGTAAATATATAAGGACTCAAAACGCGTGGAAATATCTATCTTTTAAACTTG 268
Qy 241 GCAGTTTCTAACTG 300
Db 269 GCAGTTTCTAACTG 328
Qy 301 CCCATGTGTAAATATCTCAATTGGACTGTACTTCTGGGGCTGTACAGTGAGACATTTTTC 360
Db 329 CCCATGTGTAAATATCTCAATTGGACTGTACTTCTGGGGCTGTACAGTGAGACATTTTTC 388
Qy 361 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 420
Db 389 AATTGCTTCTGACTGTGCAAGGTACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 448
Qy 421 GCCAGAGGAGGGTGCCTCTGGCATCATTAACAAGTGTCTCTGGCATGGGTAACAGCCATT 480
Db 449 GCCAGAGGAGGGTGCCTCTGGCATCATTAACAAGTGTCTCTGGCATGGGTAACAGCCATT 508
Qy 481 CTGGCCACTTTGGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG 540
Db 509 CTGGCCACTTTGGCTGAATTCGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAATACAAG 568
Qy 541 TGTGCATTTAGCAGAACTCCCTCTCCGCACTGTAGACATTCGGAAGCAATTTCTG 600

Db 569 TGTGCAATTTAGCAGAACTCCCTTCTCCGACGTGATGAGACATTCGGAAGCAATTTCTG 628
Qy 601 ACTTTAAAAATGAACATTTCCGTTCTTCTCCCTTATTTATTTTACATTTCTCTAT 660
Db 629 ACTTTAAAAATGAACATTTCCGTTCTTCTCCCTTATTTATTTTACATTTCTCTAT 688
Qy 661 GTGCAATGAGAAAAACACTAAGTTTACGAGAGCAGGATAGCCTTTTCAAGCTTGT 720
Db 689 GTGCAATGAGAAAAACACTAAGTTTACGAGAGCAGGATAGCCTTTTCAAGCTTGT 748
Qy 721 TTGCGCGTAATGGTAGTCTCTCTCTGATGTGGGCGCCCTCAATATTGCAATTTTCTG 780
Db 749 TTGCGCAATGAGTAGTCTCTCTCTGATGTGGGCGCCCTCAATATTGCAATTTTCTG 808
Qy 781 TCCACTTTCAAGAACACTTTCTCCCTGAGTGCAGAGCAGCTACAATCTCGACAAA 840
Db 809 TCCACTTTCAAGAACACTTTCTCCCTGAGTGCAGAGCAGCTACAATCTCGACAAA 868
Qy 841 AGTGTTCACATCACTAACTCATGCCACCACTGCTGCTGATCAACCCCTCTCTGTAT 900
Db 869 AGTGTTCACATCACTAACTCATGCCACCACTGCTGCTGATCAACCCCTCTCTGTAT 928
Qy 901 GCGTTTCTTGATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGTAGTAAC 960
Db 929 GCGTTTCTTGATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGTAGTAAC 988
Qy 961 ACCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGAAGAACCTTGACCAT 1020
Db 989 ACCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGAAGAACCTTGACCAT 1048
Qy 1021 TCCACCGAAGTGTA 1035
Db 1049 TCCACCGAAGTGTA 1063

RESULT 13

US-10-223-087-15
; Sequence 15, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Wellan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PlC4
; CURRENT APPLICATION NUMBER: US/10/223,087
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06566
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-087-15


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Qy 209 CTTATCCTCGTAAATATAAAGGACTCAACCGCTGGAAATATCTATCTTCTAAACTTG 268
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Qy 241 GCAGTTTCTAACTTGTGTTCTTCTGCTTACCTTCCCTTCTGCGCTCATGCTGGGGGGAT 300
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Qy 269 GCAGTTTCTAACTTGTGTTCTTCTGCTTACCTTCCCTTCTGCGCTCATGCTGGGGGGAT 328
Db |||||||
Qy 301 CCCATGTGTAATTTCTCATTGGAGTGTACCTTCTGCGCTGTACAGTGAGACATTTTTC 360
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Qy 329 CCCATGTGTAATTTCTCATTGGAGTGTACCTTCTGCGCTGTACAGTGAGACATTTTTC 388
Db |||||||
Qy 361 AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420
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Qy 389 AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 448
Db |||||||
Qy 421 GCCAGGAGGGGTGCCCTGTGGCATCTATTAAGTGTCTGGCATGGGTAAAGCCATT 480
Db |||||||
Qy 449 GCCAGGAGGGGTGCCCTGTGGCATCTATTAAGTGTCTGGCATGGGTAAAGCCATT 508
Db |||||||
Qy 481 CTGCCCACTTTGCTGAATTCGTGTTTATAAACCCTAGATGGAAGACCAAGAAATACAAG 540
Db |||||||
Qy 509 CTGCCCACTTTGCTGAATTCGTGTTTATAAACCCTAGATGGAAGACCAAGAAATACAAG 568
Db |||||||
Qy 541 TGTGCATTTAGCAGAATCCCTTCTGCGAGCTGATGAGACATTTCTGGAAGCAATTTCTG 600
Db |||||||
Qy 569 TGTGCATTTAGCAGAATCCCTTCTGCGAGCTGATGAGACATTTCTGGAAGCAATTTCTG 628
Db |||||||
Qy 601 ACTTTAAATGAACATTTGGTCTTGTCTCCCTCTATTTATTTTACATTTCTCTAT 660
Db |||||||
Qy 629 ACTTTAAATGAACATTTGGTCTTGTCTCCCTCTATTTATTTTACATTTCTCTAT 688
Db |||||||
Qy 661 GTGCAATGAGAAACACTAAGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
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Qy 689 GTGCAATGAGAAACACTAAGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 748
Db |||||||
Qy 721 TTTGCCGTATGTTAGTCTTCTCTGATGTGGCGCCCTACAATATTGCAATTTTCTCTG 780
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Qy 749 TTTGCCGTATGTTAGTCTTCTCTGATGTGGCGCCCTACAATATTGCAATTTTCTCTG 808
Db |||||||
Qy 781 TCCACTTTCAAGAACACTTCTCCTGAGTGTGCAAGAGCAGCTACAATCTGGACAAA 840
Db |||||||
Qy 809 TCCACTTTCAAGAACACTTCTCCTGAGTGTGCAAGAGCAGCTACAATCTGGACAAA 868
Db |||||||
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Db |||||||
Qy 869 AGTGTTCACATCACTAAATCTCATGCCACCACTGCTGTCATCAACCTCTCTCTGAT 928
Db |||||||
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Db |||||||
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Db |||||||
Qy 961 ACCCACTTCAACCCAGGGGAGTGTGCAAGAGCAGCTGAGGGAAGAACTTGAACAT 1020
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Qy 989 ACCCACTTCAACCCAGGGGAGTGTGCAAGAGCAGCTGAGGGAAGAACTTGAACAT 1048
Db |||||||
Qy 1021 TCCACCGAAGTGTAA 1035
Db |||||||
Qy 1049 TCCACCGAAGTGTAA 1063
Db |||||||
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RESULT 15

US-10-223-089-15

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; Sequence 15, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
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```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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FILE REFERENCE: P3235P19

CURRENT APPLICATION NUMBER: US/10/223.089

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 10/081,056

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/213,637

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/219,556

PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/220,624

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/220,664

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/222,695

PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: US 09/643,657

PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: PCT/US00/23522

PRIOR FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
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SEQ ID NO 15

LENGTH: 1475

TYPE: DNA

ORGANISM: Homo sapiens

US-10-223-089-15

Query Match

Best Local Similarity 99.7%; Score 1031.8; DB 15; Length 1475;

Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 ATGCCCAATTACAGCTGGCCAGCAGAGGATGAATATGATCTCTCATAGAGGTGAAGCTG 60
Db |||||||
Qy 29 ATGCCCAATTACAGCTGGCCAGCAGAGGATGAATATGATCTCTCATAGAGGTGAAGCTG 88
Db |||||||
Qy 61 GAGAGCGATCAGGCAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCCAGCTG 120
Db |||||||
Qy 89 GAGAGCGATCAGGCAGAGCAATGTGACAAAGTATGACGCCAGGCACTCTCAGCCCAGCTG 148
Db |||||||
Qy 121 GTGCCATCACTCTGCTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180
Db |||||||
Qy 149 GTGCCATCACTCTGCTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 208
Db |||||||
Qy 181 CTTATCCTGTAATAATATAAAGGACTCAAAAGGCTGAAATATCTATCTTCTTAAACTTG 240
Db |||||||
Qy 209 CTTATCCTGTAATAATATAAAGGACTCAAAAGGCTGAAATATCTATCTTCTTAAACTTG 268
Db |||||||
Qy 241 GCAGTTTCTAACTTGTGTTTCTTGTCTTACCTCTGCGCTTCTGCGCTCATGCTGGGGGGAT 300
Db |||||||
Qy 269 GCAGTTTCTAACTTGTGTTTCTTGTCTTACCTCTGCGCTTCTGCGCTCATGCTGGGGGGAT 328
Db |||||||
Qy 301 CCCATGTGTAATTTCTCATTGAGCTGTACTTCTGCGGCTGTACAGTGAGACATTTTTC 360
Db |||||||
Qy 329 CCCATGTGTAATTTCTCATTGAGCTGTACTTCTGCGGCTGTACAGTGAGACATTTTTC 388
Db |||||||
Qy 361 AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420
Db |||||||
Qy 389 AATTGCCCTTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 448
Db |||||||
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Qy	421	GCAGGAGGAGGTGCCCTGTGGCATCATTAAGA	480
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Qy	481	CTGGCCACTTTGGCTGAATTCGTGGTTTATAA	540
Db	509	CTGGCCACTTTGGCTGAATTCGTGGTTTATAA	568
Qy	541	TGTGCATTTAGCAGAACTCCCTTCGCCAGCTG	600
Db	569	TGTGCATTTAGCAGAACTCCCTTCGCCAGCTG	628
Qy	601	ACTTTAAATGAACATTTTCGGTTCCTTGCTC	660
Db	629	ACTTTAAATGAACATTTTCGGTTCCTTGCTC	688
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Db	689	GTGCAATGAGAAAAACACTAAGGTTTCAGGAG	748
Qy	721	TTTGGCGTAATGGTAGTCTTCCTTCTGATGTG	780
Db	749	TTTGGCCATAATGGTAGTCTTCCTTCTGATGTG	808
Qy	781	TCCACTTTCAAAGAACACTTCTCCCTGAGTGAC	840
Db	809	TCCACTTTCAAAGAACACTTCTCCCTGAGTGAC	868
Qy	841	AGTGTTCCACATCACTAAACTCATCGCCACCA	900
Db	869	AGTGTTCCACATCACTAAACTCATCGCCACCA	928
Qy	901	GGGTTTCTTGATGGGACATTTAGCAATACCTC	960
Db	929	GGGTTTCTTGATGGGACATTTAGCAATACCTC	988
Qy	961	ACCCCACTTCAACCCAGGGGGAGTCTGCACA	1020
Db	989	ACCCCACTTCAACCCAGGGGGAGTCTGCACA	1048
Qy	1021	TCCACCGAAGTGTA 1035	
Db	1049	TCCACCGAAGTGTA 1063	

Search completed: June 18, 2005, 15:44:32
Job time : 728.252 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:38:50 ; Search time 4139.74 Seconds
(without alignment)
9558.019 Million cell updates/sec

Title: US-10-623-472-32

Perfect score: 1083

Sequence: 1 atggaataactacacagtgc.....aaaggcaggataataataa 1083

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1081.4	99.9	2111	3 AK007808	Mus muscu
2	770.6	71.2	885	4 BI082667	602878081
3	684.2	61.3	958	4 BI408316	602962210
4	604.6	55.8	770	7 CV118408	AGENCOURT
5	585.8	54.1	810	2 BE911886	B5911886
6	536.6	49.5	801	7 CO425383	UI-M-HUO-
7	535.4	49.4	700	4 BG863198	602796680
8	529	48.8	540	4 BM247265	K0749D08-
9	490.4	45.3	721	7 CK839171	UI-R-AA1-
10	464.4	42.9	474	1 AI876375	uk74c03.y
11	434	40.1	615	2 BF662034	maa77f10.
12	425.6	39.3	721	6 CB598882	AGENCOURT
13	424.4	39.2	554	6 CA578957	K0730H02-
14	406.6	37.5	552	6 CA580283	K0749D08-
15	397.4	36.7	526	6 CA578095	K0732G02-
16	381.8	36.2	548	4 BI295780	UI-R-DK0-
17	388.4	35.9	518	6 CA580252	K0748H09-
18	377.4	34.8	408	5 BX631033	UI-M-BH1-
19	356.2	32.9	409	2 BE864135	602894084
20	303.4	28.0	697	4 BI107633	602894084
21	300.2	27.7	729	6 CD370587	UI-H-FT1-
22	289.4	26.7	789	6 CD466479	Leukon2_4
23	288	26.6	768	6 CD468404	Leukos3_3
24	275.8	25.5	736	6 CD466140	Leukon2_2

C	25	275.2	25.4	773	7	CO959196	CO959196	AGENCOURT
26	271	25.0	288	1	AA034646	mh17d07.x		
27	271	25.0	313	5	BX520969	BX520969		
28	270	24.9	398	6	CA579833	K0743A02-		
29	266.8	24.6	896	5	BQ892457	BQ892457	AGENCOURT	
30	264.4	24.4	749	6	CD468632	Leukos3_4		
31	263.8	24.4	724	6	CD469405	Leukos2_3		
32	263.6	24.3	673	6	CD466424	Leukon2_4		
33	262.4	24.2	654	6	CD466568	Leukon2_7		
34	262.4	24.2	664	6	CD470054	Leukos4_1		
35	262.4	24.2	691	6	CD468594	Leukos3_4		
36	260.4	24.0	650	6	CD467795	Leukos1_7		
37	259.8	24.0	370	5	BY216070	BY216070		
38	257.6	23.8	683	6	CD535056	LeukonS_3		
39	256.8	23.7	702	6	CD468196	Leukos3_1		
40	256.2	23.7	623	6	CD471186	Leukos5_1		
41	255.2	23.6	716	7	CF147784	AGENCOURT		
42	247.2	22.8	692	7	CN786392	CN786392	4120380.B	
43	242.8	22.4	793	6	CD466229	CD466229	Leukon2_2	
44	242	22.3	336	5	BY218869	BY218869		
C	45	240	22.2	413	1	AI707080	UI-R-AA1-	

ALIGNMENTS

RESULT 1	AK007808	2111 bp	linear	HTC 03-APR-2004
LOCUS	AK007808	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length		
DEFINITION	AK007808	enriched library, clone:1810047105 product:chemokine (C-C) receptor 1.-like 2, full insert sequence.		
ACCESSION	AK007808	1 GI:12841594		
VERSION	AK007808	HTC; CAP trapper.		
KEYWORDS	AK007808	Mus musculus (house mouse)		
SOURCE	AK007808	Mus musculus		
ORGANISM	AK007808	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1	Carninci, P. and Hayashizaki, Y.		
AUTHORS	1	High-efficiency full-length cDNA cloning		
TITLE	1	Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL	1	99279253		
MEDLINE	1	10349636		
PUBMED	1	10349636		
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS	2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
TITLE	2	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	2	20499374		
MEDLINE	2	11042159		
PUBMED	2	11042159		
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitagawa, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, S., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Toga, Y., Izawa, M., Ohara, S., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
AUTHORS	3	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
TITLE	3	Genome Res. 10 (11), 1757-1771 (2000)		
JOURNAL	3	20530913		
MEDLINE	3	11076861		
PUBMED	3	11076861		
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
AUTHORS	4	Functional annotation of a full-length mouse cDNA collection		
TITLE	4	Nature 409, 685-690 (2001)		
JOURNAL	4			
REFERENCE	5	The FANTOM Consortium and the RIKEN Genome Exploration Research		
AUTHORS	5			

Qy	711	GTACGACCTCCA--CAAGCGGCTCTTGTCTATAACGGGCGTGTTC--TTTGTATGTGGG 766
Db	871	GTACGACCTCCAACAAAGCGGGTCTTGTCTATAACGGGCGTGTTCCTTTTCGATGTGGG 930
Qy	767	CGCCTT-ACAACACTGTGCTTTTCC 790
Db	931	CGCCTTAACAACCTGTGCTTTTC 955
RESULT 4		
LOCUS	CV116408	770 bp mRNA linear EST 30-AUG-2004
DEFINITION	AGENCOURT 31539783 NIH_MGC_270 Rattus norvegicus cDNA clone	
	IMAGE:7445010 5', mRNA sequence.	
ACCESSION	CV116408	
VERSION	CV116408.1 GI:51635215	
KEYWORDS	EST.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
	Rattus.	
	1 (bases 1 to 770)	
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.	
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)	
TITLE	Unpublished (1999)	
JOURNAL	Contact: Daniela S. Gerhard, Ph.D.	
COMMENT	Office of Cancer Genomics	
	National Cancer Institute / NIH	
	Bldg. 31 Rm10A07 Bethesda, MD 20892	
	Email: cgabs-r@mail.nih.gov	
	Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical	
	College of Wisconsin	
	CDNA Library Preparation: Open Biosystems	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: Agencourt Bioscience Corporation	
	Clone distribution: MGC clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LLNL at:	
	http://image.llnl.gov	
	Plate: LLAM15745 row: j column: 16	
	High quality sequence stop: 713.	
FEATURES	Location/Qualifiers	
source	1..770	
	/organism="Rattus norvegicus"	
	/mol_type="mRNA"	
	/db_xref="taxon:10116"	
	/clone="IMAGE:7445010"	
	/tissue_type="whole placenta, 2 pooled"	
	/lab_host="DH10B Tona"	
	/clone_lib="NIH_MGC_270"	
	/note="Organ: placenta; Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI; Tissue was collected from two pooled placentas from the 21st day of pregnancy. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1.25 kb fragments for an average insert size of 2.15 kb. Library was normalized to Cot7. A non-normalized version of this library is also available (NIH_MGC_269). Library was constructed by Open Biosystems (Huntsville, AL). Note: this is a Mammalian Gene Collection library"	
ORIGIN		
Query Match	55.8%;	Score 604.6; DB 7; Length 770;
Best Local Similarity	88.0%;	Pred. No. 5.4e-166;
Matches	669; Conservative	0; Mismatches 90; Indels 1; Gaps 1;
Qy	47	TCTTAGCAGCTACTCTGGACACAGTGGCGCGGACCAAGTTCCGGCCCCCGAGTTCCTCT 106
Db	4	TCATAGAGGTATGACCTGGACACAGTGGGACACACCAAGTTCACACCCCGAGTTCCTCT 63
Qy	107	CCCCCAGCAGGTGTGTCAGTTCCTGTCGCGGTGTTTTCGCGGTGTTTCTCTTGACCAACG 166

CO425383	CO425383	801 bp	mRNA	linear	EST 06-JUL-2004
LOCUS	UI-M-HUO-cra-i-17-0-UI.r1 NIH_BMAP_HU0 Mus musculus cDNA clone				
DEFINITION	IMAGE:30670960 5', mRNA sequence.				
ACCESSION	CO425383				
VERSION	CO425383.1	GI:49671677			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 801)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Dr. James Lin University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP)				
Seq primer:	pyX-5.				
FEATURES	Location/Qualifiers				
source	1. .801				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="C57BL/6"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:30670960"				
	/tissue_type="whole eye"				
	/dev_stage="newborn (1, 5, 15 days)"				
	/lab_host="DH10B (T1 phage resistant)"				
	/clone_lib="NIH_BMAP_HU0"				
	/notes="Organ: Eye; Vector: pyX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AATAATTACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."				
ORIGIN					
Query Match	49.5%;	Score 536.6;	DB 7;	Length 801;	
Best Local Similarity	98.9%;	Pred. No. 5.4e-146;			
Matches 539;	Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	ATGATAACTACACAGTGGCCCCGGACGATGAATATGATCTCTTAATCTTAGACGACTAC	60		
DB	246	ATGATAACTACACAGTGGCCCCGGACGATGAATATGATCTCTTAATCTTAGACGACTAC	305		
QY	61	CTGACACACAGTGGCGCGGACCAAGTTCCGCCCCCGAGTTCCTCTCCCCCAGCAGGTG	120		
DB	306	CTGACACACAGTGGCGCGGACCAAGTTCCGCCCCCGAGTTCCTCTCCCCCAGCAGGTG	365		
QY	121	CTGCAGTCTTCCTCGCGGGTGTTCGGGTGGGTCTCTTGACACACGTCGTGGCGGTGTTT	180		
DB	366	CTGCAGTCTTCCTCGCGGGTGTTCGGGTGGGTCTCTTGACACACGTCGTGGCGGTGTTT	425		
QY	181	ATCTTGTGAAATACAAAGACATCAAGAAATCTGGGGAAACATCTTCTCTTAAACCTGGCA	240		
DB	426	ATCTTGTGAAATACAAAGACATCAAGAAATCTGGGGAAACATCTTCTCTTAAACCTGGCA	485		
QY	241	CTTTCAAACTGTGTTTCTCTGCTTCCCTGCGCTTCCCTGCGCCCACTACTGCAGCACACGGG	300		
DB	486	CTTTCAAACTGTGTTTCTCTGCTTCCCTGCGCTTCCCTGCGCCCACTACTGCAGCACACGGG	545		
QY	301	GAAAGCCCTGGCAACCGGACCTGTAAAGTTCTTGTCCGACTCCCTCGGCTTTATAC	360		
DB	546	GAAAGCCCTGGCAACCGGACCTGTAAAGTTCTTGTCCGACTCCCTCGGCTTTATAC	605		
QY	361	AGCGAGTGTGTTTCCCAACATCCCTCCCTGTCGAGGATACAGGCTGTTTCCCAAGGG	420		
DB	606	AGCGAGTGTGTTTCCCAACATCCCTCCCTGTCGAGGATACAGGCTGTTTCCCAAGGG	665		
QY	421	CGACTGGCTCCATCTTTCACGACAGTGTCTTGTGGTATTGTCGTCGATCCCTGGCATGG	480		
DB	666	CGACTGGCTCCATCTTTCACGACAGTGTCTTGTGGTATTGTCGTCGATCCCTGGCATGG	725		
QY	481	GCCATGGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTATGAGCTCGGATGGAAGA	540		
DB	726	GCCATGGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTATGAGCTCGGATGGAAGA	785		
QY	541	CAGAA 545			
DB	786	CAGAA 790			
RESULT 7					
LOCUS	BG863198	700 bp	mRNA	linear	EST 29-MAY-2001
DEFINITION	602796680F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917762 5', mRNA sequence.				
ACCESSION	BG863198				
VERSION	BG863198.1	GI:14213736			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 700)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM10829 row: p column: 19 High quality sequence stop: 700.				
FEATURES	Location/Qualifiers				
source	1. .700				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="NMRI"				
	/db_xref="taxon:10090"				
	/clone="IMAGE:4917762"				
	/tissue_type="tumor, gross tissue"				
	/dev_stage="5 months"				
	/lab_host="DH10B"				
	/clone_lib="NCI_CGAP Mam4"				
	/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."				
ORIGIN					
Query Match	49.4%;	Score 535.4;	DB 4;	Length 700;	

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Best Local Similarity 99.8%; Pred. No. 1.2e-145;
Matches 536; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 547 CACAAGTGTGCTTTGGCAAACTCCTCTTCCCAATCGAAGCGCCCTCTGGAAGTAC 606
Db 13 CACAAGTGTGCTTTGGCAAACTCCTCTTCCCAATCGAAGCGCCCTCTGGAAGTAC 72
Qy 607 GTTCTGAGCTCAAAAATGATCATCTTGGTACTTGTCTTTTCTCTGCTGCTGTTTATATC 666
Db 73 GTTCTGAGCTCAAAAATGATCATCTTGGTACTTGTCTTTTCTCTGCTGCTGTTTATATC 132
Qy 667 TGCTGCAGGCAACTGAGAGAGGAGGAGCTTCAGGAGAGACAGTACGACTCCACAAG 726
Db 133 TGCTGCAGGCAACTGAGAGAGGAGGAGCTTCAGGAGAGACAGTACGACTCCACAAG 192
Qy 727 CCGGCTCTTGTATACACGGGGGTGTTCTTTTGTATGTCGGGCGCTTACAACTGTGCTT 786
Db 193 CCGGCTCTTGTATACACGGGGGTGTTCTTTTGTATGTCGGGCGCTTACAACTGTGCTT 252
Qy 787 TTCTGTCTGCTTTCCAGGAACACTTGTCTCTGAGGATGAGAAGAGCAGCTACCACTG 846
Db 253 TTCTGTCTGCTTTCCAGGAACACTTGTCTCTGAGGATGAGAAGAGCAGCTACCACTG 312
Qy 847 GACGAAGTGTTCAGTACACAGCTGTAGCAGCACCCACCTGCTGCTGCTCAACCCGCTG 906
Db 313 GACGAAGTGTTCAGTACACAGCTGTAGCAGCACCCACCTGCTGCTGCTCAACCCGCTG 372
Qy 907 CTCTATTGCTCTTACCGGAAGCGCTTTATGATACCTTTCGAGCCTGTTCACCGG 966
Db 373 CTCTATTGCTCTTACCGGAAGCGCTTTATGATACCTTTCGAGCCTGTTCACCGG 432
Qy 967 TGCAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCGCCTCCAAAGGAAGT 1026
Db 433 TGCAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCGCCTCCAAAGGAAGT 492
Qy 1027 CATGGCAGGCCATTTGAATCTGACGCAATTTGATCAAGGCGAGGATATATATAA 1083
Db 493 CATGGCAGGCCATTTGAATCTGACGCAATTTGATCAAGGCGAGGATATATATAA 549

RESULT 8
BM247265/c 540 bp mRNA linear EST 07-JUN-2003
LOCUS K0749D08-3 NIA Mouse Hematopoietic Stem Cell (Lin-/C-Kit-/Sca-1-)
DEFINITION cDNA Library (Long) Mus musculus cDNA clone NIA:K0749D08
IMAGE:30078283 3', mRNA sequence.
ACCESSION BM247265
VERSION BM247265.2 GI:31502059
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 540)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL MEDLINE
PUBMED 11544199
COMMENT On Dec 17, 2001 this sequence version replaced gi:17882535.
Other ESTs: K0749D08-5N
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0749 row: D column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 540
POLYA=yes. Location/Qualifiers
```

source

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1. 540
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6NCr"
/db_xref="niaEST:K0749D08-3"
/db_xref="taxon:10090"
/clones="NIA:K0749D08 IMAGE:30078283"
/tissue_type="Hematopoietic Stem Cell"
/Lin-/C-Kit-/Sca-1-
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
/clone_lib="NIA Mouse Hematopoietic Stem Cell"
(Lin-/C-Kit-/Sca-1-) cDNA Library (Long)
/notes="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTTCTTTT-3'] from
0.9 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lene-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."
```

Query Match 48.8%; Score 529; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 8.2e-144; Mismatches 0; Indels 0; Gaps 0;
Matches 529; Conservative 0;

Qy 555 TGCCTTTGGCAAACTCCTCTTCCCAATCGAAGCGCGCTCTGGAAGTACGTTCTGAC 614
Db 540 TGCCTTTGGCAAACTCCTCTTCCCAATCGAAGCGCGCTCTGGAAGTACGTTCTGAC 481
Qy 615 GTCAAAAATGATCATCTTGGTACTTGTCTTCTCTGCTGCTTTTATAATCTGCTGAG 674
Db 480 GTCAAAAATGATCATCTTGGTACTTGTCTTCTCTGCTGCTTTTATAATCTGCTGAG 421
Qy 675 GCACTGAGGAGGAGGAGGAGCTTCAGGAGAGACAGTACGACTCCACAGCGCGCTCT 734
Db 420 GCACTGAGGAGGAGGAGGAGCTTCAGGAGAGACAGTACGACTCCACAGCGCGCTCT 361
Qy 735 TGTCAATACGGGCGTGTCTTCTTTGATGTGGCGCCTTACAACTGTGCTTTTCTGTC 794
Db 360 TGTCAATACGGGCGTGTCTTCTTTGATGTGGCGCCTTACAACTGTGCTTTTCTGTC 301
Qy 795 TGCTTTCCAGGAACACTTGTCTTCCCTGCAAGATGAGAAGAGAGCTACCACTTGGAGCGAAG 854
Db 300 TGCTTTCCAGGAACACTTGTCTTCCCTGCAAGATGAGAAGAGAGCTACCACTTGGAGCGAAG 241
Qy 855 TGTTCAAGTACACAGCTGTGAGCACCCACTGCTGGTCAACCGCTGCTCTATTT 914
Db 240 TGTTCAAGTACACAGCTGTGAGCACCCACTGCTGGTCAACCGCTGCTCTATTT 181
Qy 915 GCTTCTTGACGGGAAGCGCTTTTATGATACCTTTCGAGCGCTGTTCACCGGTGCAATGA 974
Db 180 GCTTCTTGACGGGAAGCGCTTTTATGATACCTTTCGAGCGCTGTTCACCGGTGCAATGA 121
Qy 975 TATCCCTATCAAGTAGTGGAGGCTATCAGCAAGCGCTTCCAAAGGAGGATCATGGAG 1034

ORIGIN

Possible reversed clone: similarity on wrong strand
 Seg primer: -40RP from Gibco
 High quality sequence stop: 397.

FEATURES

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1. 474
location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="TAOx:10090"
/cd_name="TAOx:1974724"
/cell_line="pituitary cell line"
/lab_host="SOLR"
/clones.lib="Schiller mouse Afr20"
/note="Organ: pituitary; Vector: (Stratagene); Site 1: EcoRI; Site 2: XbaI"
cdna was prepared from cell line
5'-GACAGAGACGACGACGAGAACAATGACTCTC
adaptor was used on the 5' end of
5'-AATTCCGCACGAG-3'. The library
went through one round of amplifi-
cation. The size of the amplified
size is 1.7 kb, with a range from
1.5 kb to 2.0 kb. This library
was constructed by Dr. Martin Sch-
(University). "
```

ORIGIN

Query Match	42.98;	Score 464.4;	DB 1;	Length 474;
Best Local Similarity	98.7%;	Pred. No. 7.8e-125;		
Matches 468;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	37	GATGTCCTAATCTTTAGACGACTACCTTGGACAAACAGTGGCGCGGACCAAGATTCGCGGCCCCC	96	
DB	1	GATGTCCTAATCTTTAGACGACTACCTTGGACAAACAGTGGCGCGGACCAAGATTCGCGGCCCCC	60	
QY	97	GAGTTCTCTCCCCCHAGCAGGTCTCTCAGTTCTCTGTCGCGCGGTGTTTGGGTGGGTCTC	156	
DB	61	GAGTTCTCTCTCCCCCHAGCAGGTCTCTCAGTTCTCTGTCGCGCGGTGTTTGGGTGGGTCTC	120	
QY	157	TTGGACAACGTGCTGGCGGTGTTTATCTCTGGTGAAATACAAAGGACATCAAGAAATCTGGGG	216	
DB	121	TTGGACAACGTGCTGGCGGTGTTTATCTCTGGTGAAATACAAAGGACATCAAGAAATCTGGGG	180	
QY	217	AACATCTACTTCTTAAACCTTGGACATTTTAAACCTGTGTTTCTGTCTCCCTTGCCTGCGTTC	276	
DB	181	AACATCTACTTCTTAAACCTTGGACATTTTAAACCTGTGTTTCTGTCTCCCTTGCCTGCGTTC	240	
QY	277	TGGGCCCATACTGCAGCACACGGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCTC	336	
DB	241	TGGGCCCATACTGCAGCACACGGGGAAAGCCCTGTCAATGGGACCTGTAAAGATCTTGTCTC	300	
QY	337	GGACTCCATCTCTCGGGCTTATACGCGAGGTGTTTTCCAAATCTCTCTCTTGTGCAA	396	
DB	301	GGACTCCATCTCTCGGGCTTATACGCGAGGTGTTATTTCCAAATCTCTCTCTTGTGCAA	360	
QY	397	GGATACAGGGTGTTTTCCCAAGGCGCACTGGCCCTCCATCTTACAGACAGTGCTCTTGTGGT	456	
DB	361	GGATACAGGGTGTTTTCCCAAGGCGCACTGGCCCTCCATCTTACAGACAGTGCTTGTGGT	420	
QY	457	ATTGTTGCGGTGCATCTCTGGCATCGGCCATCGGCTACTGCGCTCTCTTTTGGCCGAG	510	
DB	421	ATTGTTGCGGTGCATCTCTGGCATCGGCCATCGGCTACTGCGCTCTCTTTTGGCCGAG	474	

[illegible]

REFERENCE
AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs, mae7f10.x1
Contact: Robert Straubeberg, ph.D.
Email: cgapbsa@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGES Consortium (info@image.lnl.gov) for further information.
MG1:1459234

FEATURES

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1. .615
/organism="Mus musculus"
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ORIGIN

Query Match	40.1%	Score 434	DB 2	Length 615
Best Local Similarity	95.5%	Pred. No. 7.3e-116		
Matches 468	Conservative 0	Mismatches 10	Indels 2	Gaps 2
Qy	1	ATCGATAACTACACAGTGGCCCCGGACGATGAATATGATGTCCTTAATCTTAGACGACTAC	60	
Db	127	ATGGAATACCTACACAGTGGCCCCGGACGATGAATATGATGTCCTTAATCTTAGACGACTAC	186	
Qy	61	CTGGACAACAGTGGCGCGGACCAAGTTCGCGCCCCCGAGTTCCTCTCCCCCCAGCAGGTG	120	
Db	187	CTGGACAACAGTGGCGCGGACCAAGTTCGCGCCCCCGAGTTCCTCTCCCCCCAGCAGGTG	246	
Qy	121	CTGCAGTTCCTGTCGCGGCTGTTTGGCGTGGTCTCTTGGACAACGTGCTCGCGGTGTTT	180	
Db	247	CTGCAGTTCCTGTCGCGGCTGTTTGGCGTGGTCTCTTGGACAACGTGCTCGCGGTGTTT	306	
Qy	181	ATCTTGGTGAATATACAAAGGACTCAAGAATCTGGGGAACTATCTACTTCTTAAACCTGGCA	240	
Db	307	ATCTTGGTGAATATACAAAGGACTCAAGAATCTGGGGAACTATCTACTTCTTAAACCTGGCA	366	
Qy	241	CTTTCAAACCTGTGTTTCCCTGCTTCCCTCGCGCTCTGGGCCCCATCTGCAGCACACGGG	300	
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Qy	301	GAAAGCCCTGGCAACGGGACCTGTAAAGTCTTTGTGGACTCCACTCCTCGGGTTATAC	360	
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Qy	361	AGCGAGGTGTTTCCAAACATCCTCCTTGTGCGCAGGATACAGGGTGTTCCTCCAGGG	420	
Db	487	AGCGAGGTGTTTACAAACATCCTTCTCTTGTGCAATGATACAGGGTGTTCCTTCCATAGG	545	
Qy	421	CGACTGGCCTCCAATCTTTCACGACAG-TGTCTTGTGGTATTGTTCGTGCACTCTCGGCATG	479	
Db	546	CGACTGGCCTCAATCTTAAACGACAGCGGTCTTGTCTGATTGTTCGTGTCATCTAGTATG	605	

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Qy 480 GGCCATGGCT 489
Db 606 GGCCATGGT 615

RESULT 12
LOCUS CB598882
DEFINITION AGENCOURT_12785094 NIH_MGC_178 Mus musculus cDNA clone
IMAGE:30295418 5', mRNA sequence.
CB598882
ACCESSION CB598882.1 GI:29516738
VERSION CB598882.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 721)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgabs-x@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM53 row: b column: 03
High quality sequence stop: 541.
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            SfiI (ggccatcgcc); Site 2: SfiI (ggcgctcgcc); cDNA
            made by oligo-dT priming and directionally cloned. 5' and
            3' adaptors were used in cloning as follows:
            5'-AAGCAGTGGTATCAACGAGGTCGTCATACGCGCGG-3' and
            5'-ATTCTAGAGCGGCGGCACATG-dT(30)NN-3'. Full-length
            enriched library was constructed using the Clontech
            Creator SMART kit and size-selected to contain the 0.5 kb
            size fraction. Library created in the laboratory of M.
            Brownstein (NIMH, NIH). Note: this is a NIH_MGC library."

ORIGIN
Query Match 39.3%; Score 425.6; DB 6; Length 721;
Best Local Similarity 93.2%; Pred. No. 2.2e-113;
Matches 466; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

Qy 1 ATGATAACTACAGTGGCCCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC 60
Db 172 ATGATAACTACAGTGGCCCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC 231
Qy 61 CTGGACAACAGTGGCCCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCAGCAGGTG 120
Db 232 CTGGACAACAGTGGCCCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCAGCAGGTG 291
Qy 121 CTGCAGTTCTGCTGCGCGGTGTTTGGCGGTGGGTCTCTTGACAACTGTCGGCGGTGTTT 180
Db 292 CTGCAGTTCTGCTGCGCGGTGTTTGGCGGTGGGTCTCTTGACAACTGTCGGCGGTGTTT 351
Qy 181 ATCTTGTTGAATACAAAGACTCAAGAACTCTGGGGAACATCTACTTCTTAACCTGGCA 240
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Qy 241 CTTTCAAACTGTGTTTCTGCTTCCCTGCGCTTGGGCCCATCTACTGACACACGGG 300
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Qy 301 GAAAGCCCTGGCAACCGGACCTGTAAAGTTCTTGTGGACTCCACCTCCTCGGGC-TTATA 359
Db 472 GAAAGCCCTGGCAACCGGACCTGTAAAGTTCTTGTGGACTCCACCTCCTCGGGC-TTATA 531
Qy 360 CAGCAGAGTGTGTTTCCAAACATCTCTCTCTCTGTGCAAGGA--TACAGGAGTGTGTTTCCAA 417
Db 532 CAGCAGAGTGTGTTTCCAAACATCTCTCTCTCTGTGCAAGGAATACAGGGGTGTTTTCNCA 591
Qy 418 GGGCGACTGGCTCCCATCTTACGACAGTGTCTTGTGGTATTGTTGGTGCATCTCGGCA 477
Db 592 GGGCGACTGGCTCCCATCTTACGACAGTGTCTTGTGGTATTGTTGGTGCATCTCGGCA 651
Qy 478 TGGGCCATGGCTACTCGCT 497
Db 652 TGGGCCATGGGCCATGGCT 671

RESULT 13
LOCUS CA578957
DEFINITION K0730H02-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
IMAGE:30076501 5', mRNA sequence.
CA578957
ACCESSION CA578957.1 GI:25127348
VERSION CA578957.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 554)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,
COMMENT Aiba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
Unpublished (2001)
Other ESTs: K0730H02-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
233 Caswell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0730 row: H column: 02
Seq primer: M13 Reverse
High quality sequence stop: 554
POLYA-No.
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        NotI; Mouse cDNA project by the Laboratory of Genetics,
        National Institute on Aging (NIA), Intramural Research
        Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
        a long-transcript enriched cDNA library (Ref. Genome Res.
        11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
        obtained from Drs. Dennis Taub, Dan Longo (National
        Institute on Aging, USA), Jonathan Keller (National Cancer
        Institute, USA). Double-stranded cDNAs were synthesized

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QY 301 GAAAGCCCTGGCAACGGACCTGTAAAGTTCTTGTGGACTCCACTCCTCGGCTTATAC 360
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 Db 440 GAAAGCCCTGGCAATGGACCTGTAAAGTTCTTGTGGACTCCACTCCTCGGCTTATAC 499
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RESULT 15
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 LOCUS
 DEFINITION K0732G02-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1-)
 cDNA Library (long) Mus musculus cDNA clone NIA:K0732G02
 IMAGE:30076681 5', mRNA sequence.

ACCESSION CA579095
 VERSION
 KEYWORDS
 SOURCE CA579095.1 GI:25127486
 EST.

ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 526)

REFERENCE Piao Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
 Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
 Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
 (Lin-/c-kit-/Sca-1-) cDNA Library (long)
 Unpublished (2001)

TITLE Other ESTs: K0732G02-3
 JOURNAL
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Plate: K0732 row: G column: 02
 Seq primer: M13 Reverse
 High quality sequence stop: 526
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 (Lin-/c-kit-/Sca-1-) cDNA Library (long)"
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 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
 obtained from Drs. Dennis Taub, Dan Longo (National
 Institute on Aging, USA), Jonathan Keller (National Cancer
 Institute, USA). Double-stranded cDNAs were synthesized
 with an Oligo(dT) primer [Invitrogen:
 5'-pGACTACTTATAGATCGAGCGCCCTTTTCTTTTCTTTT-3'] from
 0.9 ug of total RNA, treated with T4 DNA polymerase, and
 purified by ethanol-precipitation. The cDNAs were ligated
 to Lona-linker LI-Sal4, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Taq polymerase (Takara) with a primer Sal4-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with Sali and NotI enzymes
 and cloned into Sali/NotI site of pSPORT1 plasmid vector.

The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.1 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN

Query Match 36.7%; Score 397.4; DB 6; Length 526;
 Best Local Similarity 99.7%; Pred. No. 4e-103; Indels 0; Gaps 0;
 Matches 398; Conservative 0; Mismatches 1;

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QY 121 CTGCAGTCTCTGCTGCGCGGTGTTTGGGTGGTCTCTTGGACAACGCTGCGGGTGT 180
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QY 181 ATCTTGGTGAATAACAAAGGACTCAAGAATCTGGGGAACATCTTCTTAAACCTGGCA 240
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Db 308 ATCTTGGTGAATAACAAAGGACTCAAGAATCTGGGGAACATCTTCTTAAACCTGGCA 367
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QY 241 CTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCGGGCCCATCTGCGACACACGGG 300
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Db 368 CTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCGGGCCCATCTGCGACACACGGG 427
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QY 301 GAAAGCCCTGGCAACGGACCTGTAAAGTTCTTGTGGACTCCACTCCTCGGCTTATAC 360
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Db 428 GAAAGCCCTGGCAATGGACCTGTAAAGTTCTTGTGGACTCCACTCCTCGGCTTATAC 487
 |||||

QY 361 AGCGAGGTGTTTCCAAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
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Db 488 AGCGAGGTGTTTCCAAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 526
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Search completed: June 18, 2005, 12:08:00
 Job time : 4144.74 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:41:10 ; Search time 208.112 Seconds
(without alignments)
8515.071 Million cell updates/sec

Title: US-10-623-472-32

Perfect score: 1083

Sequence: 1 atggtactactacacagtgc.....aaaggcaggataataataa 1083

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	421.6	38.9	1270	4	US-09-016-434-756 Sequence 756, App
2	420.4	38.8	1547	4	US-10-039-659A-11 Sequence 11, Appl
3	398.4	36.8	1050	3	US-08-681-192-1 Sequence 1, Appl
4	184.8	17.1	1059	4	US-08-771-276-19 Sequence 19, Appl
5	183.2	16.9	1065	3	US-08-847-296B-2 Sequence 2, Appl
6	183.2	16.9	1068	4	US-08-826-509-474 Sequence 474, App
7	183.2	16.9	1139	4	US-08-375-199B-3 Sequence 3, Appl
8	183.2	16.9	1193	4	US-08-720-565-3 Sequence 3, Appl
9	183.2	16.9	1201	4	US-08-016-434-1085 Sequence 1085, App
10	183.2	16.9	1201	4	US-09-023-655-905 Sequence 905, App
11	183.2	16.9	1717	4	US-08-023-655-959 Sequence 959, App
12	183.2	16.9	1915	3	US-08-575-967A-3 Sequence 3, Appl
13	183.2	16.9	1915	4	US-08-771-276-3 Sequence 3, Appl
14	180	16.6	1689	4	US-08-720-565-1 Sequence 1, Appl
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20	178.6	16.5	1059	3	US-08-724-984A-3 Sequence 3, Appl
21	178.6	16.5	1225	4	US-09-023-655-967 Sequence 967, App
22	178.6	16.5	1376	3	US-09-087-232A-12 Sequence 12, Appl
23	178.6	16.5	1376	4	US-09-016-434-1104 Sequence 1104, App
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28	178.6	16.5	1414	4	US-09-195-662A-1 Sequence 1, Appl
29	178.6	16.5	1477	3	US-08-833-752-2 Sequence 2, Appl
30	178.6	16.5	1477	4	US-09-938-719-2 Sequence 2, Appl
31	178.6	16.5	1477	4	US-09-939-226B-2 Sequence 2, Appl
32	178.6	16.5	3383	3	US-08-861-105-13 Sequence 13, Appl
33	178.6	16.5	3383	3	US-08-575-967A-1 Sequence 1, Appl
34	178.6	16.5	3383	4	US-09-023-655-951 Sequence 951, App
35	178.6	16.5	3383	4	US-08-771-276-1 Sequence 1, Appl
36	178.6	16.5	5674	4	US-09-293-170-3 Sequence 3, Appl
37	177	16.3	1059	3	US-08-826-509-476 Sequence 476, App
38	177	16.3	1071	3	US-09-087-232A-14 Sequence 14, Appl
39	175.2	16.2	1414	3	US-08-486-343D-1 Sequence 1, Appl
40	173.8	16.0	1059	3	US-09-517-605-8 Sequence 8, Appl
41	167.4	15.5	1495	4	US-09-016-434-1190 Sequence 1190, App
42	167.4	15.5	1495	4	US-09-023-655-1021 Sequence 1021, App
43	167.4	15.5	2156	1	US-08-012-988A-1 Sequence 1, Appl
44	167.4	15.5	2156	4	US-09-023-655-1247 Sequence 1247, App
45	158	14.6	2772	4	US-09-919-039-171 Sequence 171, App

ALIGNMENTS

RESULT 1
US-09-016-434-756
; Sequence 756, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 756:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MPHGN03
; CLONE: 442279
; US-09-016-434-756

Query Match 38.9%; Score 421.6; DB 4; Length 1270;
Best Local Similarity 65.4%; Pred. No. 1.5e-124;

Matches 708; Conservative 1; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGATAACTACAGTGGCCCGGACGATGAATATGATCTCTAATCTTAGACGACTAC 60
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180 ATGGCCAATTACACGCTGGCCACGAGGATGAATATGATGTCC---TCATAGAAGGTGAA 236
Qy 61 CTGGACAACAGTGGCGGACCAAGTT-----CCGGCCCCGAGTTCCTCTCCCCCAG 114
Db |||||
237 CTGGAGAGCGATGAGGAGAGCAATGTGACAAGTATGACCCCGAGGACTCTCAGCCCG 296
Qy 115 CAGGTGCTGCAGTCTCTCGCGGGTGTTCGCGGTCTCTTGGACAACGTCGTGGCG 174
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297 CTGGTGCCATCACTCTGCTCTGCTGTGTGTGTGATCGTCTCTGGACAATCTCTGGTT 356
Qy 175 GTGTTTATCTTGTGAAATACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 234
Db |||||
357 GTGCTTATCTGTGTAATAATAAGGACTCAAAAGCGGTGGAATAATCTATCTTCTAAAC 416
Qy 235 CTGGCACTTTCAACCTGTCTTCTGCTTCCCTGCTCCGCTTCTGGGCCCATCTAGCAGCA 294
Db |||||
417 TTGGCAGTTTCACTTGTGTGTCTTCTTACCTCGCCCTCTGGGCTCATGCTG----- 471
Qy 295 CACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGCGACTCCACTCTCGGGC 354
Db |||||
472 -----GGGCGATCCCATGTGTGTAATAATCTCATTTGACTGTACTTCTCGGGC 518
Qy 355 TTATACAGCAGGTGTTTTCACATCTCTCTCTGTGTGCAAGGATACAGGGTGTTC 414
Db |||||
519 CTGTACAGTGAGACAVTTCATTTGCTTCTGACTGTGCAAGGTACCTAGTGTTC 578
Qy 415 CAAGGGCGAC---TGGCCTCCATCTTCACGACAGTGTCTGTGTATGTTGTGCGTCATC 471
Db |||||
579 CACAAGGGCAACTTTTCTCAGCAGGAGGAGGCGCTGTGGCATTAACAAGTTC 638
Qy 472 CTGGCATGGCCATGGCTACTGGGCTCTCTTTCGCCGAGTCTGTGTTTATGACCTCGG 531
Db |||||
639 CTGGCATGGTAAACAGCAATCTGGCCACTTGGCTGAATACGTGTTTATAACCTCAG 698
Qy 532 ATGGAAGAAGACAGAAACAAGTGTGCTTTGGCAAACTCACTTCTTGGCAATCGAAGCG 591
Db |||||
699 ATGGAAGACAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAG 758
Qy 592 CCGCTCTGGAAGTACGTCTGACGTCAAAATGATCATCTTGTGTACTGTTTCTCTG 651
Db |||||
759 ACATCTGGAAGCAATTTCTGACTTTTAAATGAACATTTGCGTCTTGTCTCTCCCTA 818
Qy 652 CTGGTTTTTATAATCTGCTGACGCAACTGAGGAGAGGAGGAGCTTCAGGGAGAGACAG 711
Db |||||
819 TTTATTTTACATTTCTCTATGTGCAATGAGAAATACTAAGGTTTCAGGGAGCAGAGG 878
Qy 712 TAGCACTTCCAAAGCCGGCTCTGTGATTAACGGGGGTGTTCTTTTGTGATGTGGGCGCT 771
Db |||||
879 TATAGCCTTTTCAAGCTGTGTTTGGCCATAATGGTAGTCTCTCTCTGATGTGGGCGCC 938
Qy 772 TAGCAACTGTGCTTTTCTGTCTGCTTCCAGCAACATTTGCTTCCCTGAGGATGAGAAG 831
Db |||||
939 TACAATATGCAATTTTCTGTGCTCACTTTCAAGAACACTTCTCCCTGAGTGAATGCAAG 998
Qy 832 AGCAGCTTACCACCTGGACGAAGTGTTCAGGTCAACAGCTGGTAGCAGCACCCACTGC 891
Db |||||
999 AGCAGCTTACAATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCACTGC 1058
Qy 892 TGGGTCAACCGGTGCTATTTGCTTCTTGAACGGAGCGCTTTATGATATACCTTCGC 951
Db |||||
1059 TGCATCAACCGCTCTCTGTATGCGTTCCTGATGGGA---CATTTAGCAATACTCTGTC 1115
Qy 952 AGCTGTCTCCAGGTCGAATGATATCCCTTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
Db |||||
1116 CGCTGTTTCAATCTGCGTAGTAACACCCACTTCAACCCAGGGGCGAGTCTGCACAAAGC 1175
Qy 1012 CCTCCAAAGGAAGTCAATGGCAGGCCCAATTTGAATGTGACGAATTTGCAATCAAGGCAG 1071
Db |||||
1176 ACATCGAGGGAAGAACTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAATGCAA 1235
Qy

Qy 1072 GA 1073
Db 1236 GA 1237

RESULT 2

US-10-039-659A-11
; Sequence 11, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589K1B US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; PRIOR FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-039-659A-11

Query Match 38.8%; Score 420.4; DB 4; Length 1547;
Best Local Similarity 65.4%; Pred. No. 4e-124;
Matches 708; Conservative 0; Mismatches 341; Indels 33; Gaps 5;

Qy 1 ATGGATAACTACAGTGGCCCGGACGATGAATATGATGTCTAATCTTAGACGACTAC 60
Db |||||
85 ATGGCCAATTACACGCTGGCACGAGGATGAATATGATGTCC---TCATAGAAGGTGAA 141
Qy 61 CTGGACAACAGTGGGCGGACCAAGTT-----CCGGCCCCGAGTTCCTCTCCCCCAG 114
Db |||||
142 CTGGAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGACTCTCAGCCCG 201
Qy 115 CAGGTGCTGCAGTCTTGTGCGCGGTGTTTGGGGTCTCTTGGACAACGTCGTGGCG 174
Db |||||
202 CTGGTGCCATCACTCTGCTCTGCTGTGTGTGTGATCGGTCTCTGGACAATCTCTGGTT 261
Qy 175 GTGTTTATCTTGGTGAATACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 234
Db |||||
262 GTGCTTATCTGGTAAATAATAAAGGACTCAAAACGGGTGGAATAATCTATCTTCTAAAC 321
Qy 235 CTGGCACTTTCAAAACCTGTGTTTCTCTGCTTCCCTGCGGCTCTGGGCCCATCTATGCA 294
Db |||||
322 TTGGCAGTTTCAACTGTGTTTCTTGTCTTACCTGCGGCTCTTGGGCTCATGCTG---- 376
Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGTCGACTCTCCTCGGCT 354
Db |||||
377 -----GGGCGCATCCCATGTGTGTAAATTTCTCATTTGGAATCTCTCTGGGCT 423
Qy 355 TTATACAGCAGGTGTTTTCACACATCTCTCTTGTGTGCAAGGATACAGGGTGTTC 414
Db |||||
424 CTGTACAGTGAGACATTTTTTCAATTCGCTTCTGACTGTGCAAGGTACCTAGTGTTC 483
Qy 415 CAAGGGCGAC---TGGCCTCCATCTTTCAGCAGACAGTGTCTTGTGTGATTTGTGCGT 471
Db

Db 484 CACAAGGCGCACTTTTCTCAGCAGGAGGAGGCTGCTGCGCATCATTTACAAGTGC 543
Qy 472 CTGCGATGGGCGCATGCTGCGTCTCTTTGCGCGAGTCTGTGTTTATGAGCCTCGG 531
Db 544 CTGCGATGGGTAACAGACCAATTCGCGCACTTTGCGTGAATTCGTGGTTTATAAACCTCAG 603
Qy 532 ATGGAAGACAGAAACACAGTGTGCTTTTGGCAAACTCACTTCTTGCCCAATCGAAGCG 591
Db 604 ATGGAAGACAGAAATACAGTGTGCTTTTACGAGAACTCCTTCTGCGCAGCTGTAG 663
Qy 592 CCGCTCTGGAAGTACGTTCTGACGTCAAAAATGATCATTTTGGTACTGCTTTTCTCTG 651
Db 664 ACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCCGTTCTTGTCTCCCTC 723
Qy 652 CTGCTTTTATAATCTCTGCGAGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 711
Db 724 TTTATTTTATCATTTCTATGTGCAATGAGAAACACTAAGGTTTCAGGAGGAGGAGG 783
Qy 712 TACGACCTCCACAAAGCGGCTTGTGTATACAGCGGCGTGTCTTTTGTGAGTGGCGCT 771
Db 784 TATAGCCTTTTCAAGCTTGTTTTGGCGTAATGTAGTCTTCTTCTGATGTGGCGGCC 843
Qy 772 TACAACACTGTCTTTTCTGCTGTCTTTCAGGAACAATTTGCTGCGAGGATGGAAG 831
Db 844 TACAATATTGCAATTTTCTGCTGCTTTCAGGAACAATTTCTCTCCCTGAGTGAAGTGA 903
Qy 832 AGCAGCTACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 891
Db 904 AGCAGCTACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 963
Qy 892 TGGCTCAACCGCTGCTCTATTTCTGCTTTCAGCGGAGGCTTTTATGAGATACCTTCGC 951
Db 964 TGCATCAACCTCTCTCTGTATGCTGCTTCTGATGCGA---CATTTAGCAATACCTCTGC 1020
Qy 952 AGCCTGTTCACCGCTGCAATGATATCCCTTATCAAAAGTGTGAGGAGGCTATCAGCAAGCG 1011
Db 1021 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGC 1080
Qy 1012 CTTCAAGGAGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1071
Db 1081 ACATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Qy 1072 GA 1073
Db 1141 GA 1142

RESULT 3

US-08-681-192-1

; Sequence 1, Application US/08681192

; Patent No. 6287801

; GENERAL INFORMATION:

; APPLICANT: BERGMA, DERK

; APPLICANT: ELSHOURBAGY, NABIL

; APPLICANT: SARAU, HENRY

; APPLICANT: RUBEN, STEVEN

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFDS78

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-2799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/681,192

; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-681-192-1

Query Match 36.8%; Score 398.4; DB 3; Length 1050;

Best Local Similarity 66.5%; Pred. No. 3.7e-117; Indels 33; Gaps 5;
Matches 662; Conservative 0; Mismatches 301;

Qy 1 ATGGAATACTACACAGTGGCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 76 ATGSCCAATTACAGCTGCGCACGAGGATGAATATGATGTCC---TCATAGAAGGTGAA 132
Qy 61 CTGGAACAAGTGGCCCGGACCAAGTT-----CCGGCCCCGAGTGTCTCTCCCCCAG 114
Db 133 CTGAGAGCGATGAGGAGGAGCAATGTGACAAGTATGACGCCAGGCACTCTCAGCCAG 192
Qy 115 CAGGTCTGCGAGTCTGCTGCGGGTGTGCGGTGGTCTCTTGGGACAACTGCTGCGG 174
Db 193 CTGGTGCATCACTCTGCTCTGCTGTGTGTGTGATCGGTGTCTTGGCAATCTCTCTGTT 252
Qy 175 GTGTTATCTTGTGTAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 234
Db 253 GTGTTATCTTGTGTAATAACAAGGACTCAAGAATCTGGGGAATACTATCTTCTTAAC 312
Qy 235 CTGGCACTTTCAAACTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
Db 313 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCTGCTCTCTCTCTCTCTCTCTCT 367
Qy 295 CACGGGGAAGCCCTGGAACGGGAGCTGTAAAGTCTTGTGCGACTCCACTCTCTCGGC 354
Db 368 -----GGGCGGATCCATGTGTAAATTTCTCATTTGGACTGTACTCTGTGGC 414
Qy 355 TTATACAGCGAGGTGTTTTCACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 412
Db 415 CTGTACAGTGAGACATTTTTCATTTGCTCTGTGCTGTGCAAGGAGTACCTAGTGTGTT 474
Qy 413 -CCCAAGGCGACTGGCCTCCATCTTCAACAGTGTCTTGTGGTATGTTGCGTCAATC 471
Db 475 CACAAGGGCAACTTTTCTCAGCAGGAGGAGGTGCTCTGTGGCATCATTTACAAGTGT 534
Qy 472 CTGGCATGGGCCCATGCTACTGCGCTCTCTTTGCGCGAGTCTGTGTTTATGAGCCCTCG 531
Db 535 CTGGCATGGGTAAAGCCATTTCTGGCCACTTTGCTGAAATTCGTGGTTTATAACCTCAG 594
Qy 532 ATGGAAGACAGAAACAACAAGTGTGCTTTTGGCAAACTCACTTCTTGGCAATCGAAGCG 591
Db 595 ATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCTGCCAGTGTAG 654
Qy 592 CCGCTCTGGAAGTACGTTCTGAGCTCAAAAATGATCATCTTGTGACTTGTCTTCTCTG 651
Db 655 ACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCCGTTCTTGTGCTCTCTCT 714

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: PatentIn Release #1.0, Version #1.30
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 92..1156
US-08-720-565-3

Query Match 16.9%; Score 183.2; DB 4; Length 1193;
Best Local Similarity 54.3%; Pred. No. 5.2e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

QY 110 CCCAGCAGGTGCTCGAGTCTGCTGCGCGGTGTTGGGTGGTCTCTTGGACAACTGC 169
DB 192 CCCAGTTGTGCCCCCGCTGACTCCCTGGTGTCTACTGTGGGCTCTTGGGCAATGG 251
QY 170 TGGCGGTGTTATCTTGGTGAATACAAAGACATCAAGATCTGGGAAATCTACTTCC 229
DB 252 TGGTGGTGATGATCCTCATAAATACAGGAGCTCCGAATATACCAACATCTACCTGC 311
QY 230 TAACTGGCACTTTCAACCTGTGTTCTGCTTCCCTGCCCTTCTGGGCCATCTG 289
DB 312 TCAACCTGGCCATTTCCGACCTGCTCTCTCTCGTCACTCTTCCATTTGGATCCACTG 371
QY 290 ---CAGCACACGGGAAAGCCCTGGCAAGGACCTGTAAAGTTCTTGTGGACTCCACT 346
DB 372 TCAGGGGGCATACTGCGGTTTTGGCCATGCGATGTGTAGCTCTCTCAGGGTTTATC 431
QY 347 CCTCGGCTTATACAGCGAGTGTGTTTCCAAATCTCTCTCTCTTGTGGAAGATACAGG 406
DB 432 ACACAGGCTTGTACAGCGAGATCTTTTTCATAATCTCTGTCGACAAATACAGAGGTACCTGG 491
QY 407 TGTTTCCCAAGGCGACTGCGCTCCATCTTTCACGACAGTGTCTTGTGTTATGTTGGT 466
DB 492 CCATTGTCCATGTGTGTTGTCCTTCCAGCCCGGACTGTCACTTTTGGTGTCAACCA 551
QY 467 GCATCTCGGATGGGCGCATGCTACTGCGCTCTCTTTCGCGAGTCTGTGTTTATGAGC 526
DB 552 GCATCTGTCATCTGGGCTGGCAGTGTAGCAGTCTCTCTGAAATTTATCTTCTATGAGA 611
QY 527 CTCGGATGGAAGACAGAAACACAAGTGTGCTTTGGCAACCTCACTTCTTGGCAATCG 586
DB 612 CT-----GAAGAGTGTGTTGAAGAGACTCTTTTGCAGTGCTCTTTTACCCAGAGATA 662
QY 587 AAGCGCGCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGGTACTGCTTTTC 646
DB 663 CAGTATATAGCTGGAGGCAATTTCCACACTCTGTGAGAAATGACCATCTTCTGCTGTTCTCC 722

647 CTCTGCTGGTTTTTATAATCTGCTGAGCAACCTGAGGAGAGGC-----AGAGCTTCA 700
DB 723 CTCTGCTGGTTATGCGCATCTGCTACACAGAAATCATCAAAACCTGCTGTAGGTGCCCCA 782
QY 701 GGGAGAGACAGTACGACCTCCACAAAGCCGCTCTTGTCTATAACGGGCGTGTCTCTTTGA 760
DB 783 GTAAAAAAGTACAAAGCCATCGGCTCATTTTTTGTCTCATATGCGGCTGTTTTTCATTT 842
QY 761 TGTGGCGCTTACAAACACTGTGCTTTTCTGCTGCTGTTTCCAGGAACACTTGTCCCTGC 820
DB 843 TCTGGACACCTACATGTTGGCTATCTTCTCTCTCTATCATCATCTTATTTGAA 902
QY 821 AGGATGAGAGAGAGACTACCACTGACGCAAGTGTTCAGGTCAACAGCTGTGAGCA 880
DB 903 ATGACTGTGAGCGGAGCAAGCATCTGGACCTGGTCTGCTGTCGACAGAGGTGATCGCCT 962
QY 881 CCACCACTGCTGGTCAACCCGCTGCTCTATTTGCTTCTTG 922
DB 963 ACTCCCACTGCTGATGACCCGCTGATCTACGCTTTGTTG 1004

RESULT 9
US-09-016-434-1085
; Sequence 1085, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1085:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1199579
; US-09-016-434-1085

Query Match 16.9%; Score 183.2; DB 4; Length 1201;
Best Local Similarity 54.3%; Pred. No. 5.3e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;

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QY 110 CCAGCAGAGTGTGACAGTCTCTGCGCGGTGTTGGGTGCTCTTGGCAACGTCG 169
Db 132 CCAGTTTGTGCCCGCTGTACTCCTCGTGTGTCACTGTGGGCTCTTGGCAATGTGG 191
QY 170 TGGCGGTGTTTATCTTGGTGAATACAAAGGACTCAAGAACTTGGGGAACATCTACTTCC 229
Db 192 TGGTGGTGAATCCTCATAAATACAGAGGCTCCGAATATGACCAACATCTACTGTC 251
QY 230 TAAACCTGGCACTTTCAAACCTGTGTCTGCTTCCCTTGGCGTCTTGGGCCCACTG 289
Db 252 TCAACCTGGCACTTGGACCTGTCTTCTCGTCAACCTTCCATCTGGATCCACTATG 311
QY 290 ---CAGCACAGGGGAAGCCCTGGCAACGGGACCTGTAAGTCTTGTGCGACTCCACT 346
Db 312 TCAGGGGGCATACTGGGTTTTGGCCATGGCATGTGTAGTCTCTCTCAGGGTTTATC 371
QY 347 CTTGGGCTTATACAGCGAGGTGTTTTCCAACTCTCTCTCTTGTGCAAGGATACAGGG 406
Db 372 ACACAGGCTTGTACAGCGAGATCTTTTTCATAATCTCTGCTGACAATCGACAGGTACCTGG 431
QY 407 TGTTCCTCCAGGGGCACTGGCTCCATCTTACAGCAGTGTCTTGTGGTATTTGTCGT 466
Db 432 CCATTTGTCAATGCTGTGTTTGGCCCTTCGAGCCCGGACTGTCTCTTGGTGTATCACC 491
QY 467 GCATCTCGCATGGGCGCATGGCTACTGCGCTCTCTTTTGGCCGAGTCTGTGTTTATGAGC 526
Db 492 GCATCTCGCATGGGCGCTGGCGCTGGCGCTCTCTGAAATTTATCTTCTATGAGA 551
QY 527 CTCGGATGGAAGACAGAAACACAAGTGTGCTTTGGCAACCTCACTCTTCCCAATCG 586
Db 552 CT-----GAAGAGTGTGTTGAAGAGACTCTTTGCACTGTCTTTTACCCAGAGGATA 602
QY 587 AAGCGCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTATCTTCTTTC 646
Db 603 CAGTATATAGCTGGAGGCAATTTCCACACTCTGTGAAGATGACCATCTTCTGTCTCTCC 662
QY 647 CTCTGCTGTTTTTATTAATCTGTCGAGGCAACTGAGGGAAGGC-----AGAGCTTCA 700
Db 663 CTCTGCTGTTATGGCCATCTGTACACAGGATCATCAAAACGCTGCTGAGTGGCCCA 722
QY 701 GGGAGAGACAGTACGACCTCCACAAGCCGCTCTTGTATPAAACGGGCGTCTCTTTTGA 760
Db 723 GTAAAAAAGATCAAGGCCATCGGCTCATTTTGTGTCATCATGGCGGTGTTTTTCATTT 782
QY 761 TGTGGGCGCTTACACACTGTGCTTTCTGCTGCTTCTGCTGCTTCCAGGAACACTTCCCTGC 820
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QY 821 AGGATGAGAAGAGCAGCTACCACTGGACGCAAGTGTTCAGGTCAACAGCTGCTAGCGA 880
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QY 881 CCACCCACTGCTGGTCAACCCGCTGCTCTATTGCTTTG 922
Db 903 ACTCCCACTGCTGATGAACCCGCTGATCTACGCCCTTTGTTG 944
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RESULT 10

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US-09-023-655-905
; Sequence 905, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
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; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: 08/09/023,655
; APPLICATION NUMBER: US/09/023,655
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 905:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1199579
; US-09-023-655-905
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Query Match 16.9%; Score 183.2; DB 4; Length 1201;
Best Local Similarity 54.3%; Pred. No. 5.3e-48;
Matches 446; Conservative 0; Mismatches 358; Indels 18; Gaps 3;
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QY 110 CCAGCAGAGTGTGACAGTCTCTGCGCGGTGTTGGGTGCTCTTGGCAACGTCG 169
Db 132 CCAGTTTGTGCCCGCTGTACTCCTCGTGTGTCACTGTGGGCTCTTGGCAATGTGG 191
QY 170 TGGCGGTGTTTATCTTGGTGAATACAAAGGACTCAAGAACTTGGGGAACATCTACTTCC 229
Db 192 TGGTGGTGAATCCTCATAAATACAGAGGCTCCGAATATGACCAACATCTACTGTC 251
QY 230 TAAACCTGGCACTTTCAAACCTGTGTGTTCTGCTGCTCCCTGCGTCTTGGGCCCACTG 289
Db 252 TCAACCTGGCACTTTCGGACCTGCTCTCTCTGTCACCTTCCATCTTGGATCCACTATG 311
QY 290 ---CAGCACAGGGGAAGCCCTGGCAACGGGACCTGTAAGTCTTGTGCGACTCCACT 346
Db 312 TCAGGGGGCATACTGGGTTTTGGCCATGGCATGTGTAGTCTCTCTCAGGGTTTATC 371
QY 347 CTTGGGCTTATACAGCGAGGTGTTTTCCAACTCTCTCTCTTGTGCAAGGATACAGGG 406
Db 372 ACACAGGCTTGTACAGCGAGATCTTTTTCATAATCTCTGCTGACAATCGACAGGTACCTGG 431
QY 407 TGTTCCTCCAGGGGCACTGGCTCCATCTTACAGCAGTGTCTTGTGGTATTTGTCGT 466
Db 432 CCATTTGTCAATGCTGTGTTTGGCCCTTCGAGCCCGGACTGTCTCTTGGTGTATCACC 491
QY 467 GCATCTCGCATGGGCGCATGGCTACTGCGCTCTCTTTTGGCCGAGTCTGTGTTTATGAGC 526
Db 492 GCATCTCGCATGGGCGCTGGCGCTGGCGCTCTCTGAAATTTATCTTCTATGAGA 551
QY 527 CTCGGATGGAAGACAGAAACACAAGTGTGCTTTGGCAACCTCACTCTTCCCAATCG 586
Db 552 CT-----GAAGAGTGTGTTGAAGAGACTCTTTGCACTGTCTTTTACCCAGAGGATA 602
QY 587 AAGCGCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTATCTTCTTTC 646
Db 603 CAGTATATAGCTGGAGGCAATTTCCACACTCTGTGAAGATGACCATCTTCTGTCTCTCC 662
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Db 462 CCCAGTTTGTGCCCCCGCTGTACTCCCTGGTGTTCACCTGTGGCCCTCTTGGCAATGTGG 521
Qy 170 TGGCGGTCTTATCTTGTGTAATACAAAGAGCTCAAGAACTGGGGAACATCTACTTCC 229
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Qy 230 TAAACCTGGCACTTTCAAACCTGTGTTTCCCTCTCCCTGCTCCGCTTCTGGGCCCATACTG 289
Db 582 TCAACCTGGCCATTTCCGACCTGTCTTCTCCTCGTCACCTTCCATCTCTGGATCCACTATG 641
Qy 290 ---CAGCACAGGGGAAGCCCTGGCAAGGAGCTGTAAAGTTCTTGTGGACTCCACT 346
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Qy 347 CTTGGGCTTATACAGCAGGTGTTTTCCAACTCTCTCTCTGTGTGCAAGATACAGGG 406
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Qy 407 TGTTTTCCAAAGGGCACTGGCCCTCCATCTTTACAGACAGTGTCTTGTGTATTTGTGGT 466
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Qy 467 GCATCTGGCATGGCCATGGCTACTCGCTCTCTTCCCGAGTGTGTGTTTTATGAGC 526
Db 822 GCATCGTCACCTGGGCGCTGGCAGTGTAGCAGCTCTTCTCGAATTTATCTTCTATGAGA 881
Qy 527 CTCGGATGAAGACAGAAACACAGAGTGTGCTTTGGCAACCTCACCTTTTGCCAATCG 586
Db 882 CT-----GAAGAGTTGTTGAAGAGCTCTTTGAGTGTCTTTTACCAGAGGATA 932
Qy 587 AAGCGCGCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGTACTTGTCTTTC 646
Db 933 CAGTATATAGCTGGAGGCAATTTCCACACTCTGAGAAATGACCATCTTCTGTCTGTCTCC 992
Qy 647 CTCTGTGGTTTTTATATCTGTGCGAGCACTGAGGAGAGGC-----AGAGCTTCA 700
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Qy 701 GGGAGAGACGTACGACCTCCACAGCGGCTCTTGTATACAGCGGCTTCTTGTGTTTGA 760
Db 1053 GTAAAAAAGTACAGGCCATCCGGCTCATTTTGTGTCATGTCGGGTGTTTTTCATTT 1112
Qy 761 TGTGGGCGCTTACAAACACTGTGTCTTCTGTCTGTCTTCCAGGAAACATTTGCTCCTGC 820
Db 1113 TCTGACACCTACATGTGGCTATCTCTCTCTCTCTATCAATCCATCTTATTTGGA 1172
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Qy 881 CCACCCACTGTGGTCAACCGGCTGCTCTATTTGCTTCTTG 922
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RESULT 14

US-08-720-565-1
; Sequence 1, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive

; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David B.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-720-565-1

Query Match 16.6%; Score 180; DB 4; Length 1689;

Best Local Similarity 54.0%; Pred. No. 7e-47;

Matches 444; Conservative 0; Mismatches 360; Indels 18; Gaps 3;

Qy 110 CCCAGCAGGTGCTCAGTCTCTGCGCGGTGTTTGGGTGGTCTCTTGGACACGTCG 169
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Qy 290 ---CAGCACAGGGGAAGCCCTGGCAACGGAGCTGTAAAGTTCTTGTTCGAGCTCCACT 346
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Qy 347 CTTGGGCTTATACAGCAGGTGTTTTCCAACTCTCTCTCTTGTGTGCAAGATACAGGG 406
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Db 932 TCTGGACACCTACAATGTGCTATCTCTCTCTCTATCAATCCATCTTATTTGGAA 991
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RESULT 15
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; Sequence 15: Application US/09931381A
; Patent No. 6692922
; GENERAL INFORMATION:
; APPLICANT: Butcher, Eugene C.
; APPLICANT: Kunkel, Eric J.
; APPLICANT: Pan, Junliang
; APPLICANT: Soler-Ferran, Dulce
; TITLE OF INVENTION: Method for Identifying Agents Which
; TITLE OF INVENTION: Modulate Chemokine "MBC"-Induced Functions of CCR3 and/or
; FILE OF INVENTION: CCR10
; FILE REFERENCE: 1855.2010-003
; CURRENT APPLICATION NUMBER: US/09/931.381A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: U.S. 09/638,914
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (181)...(1248)
; NAME/KEY: misc feature
; LOCATION: (1291)...(1291)
; OTHER INFORMATION: n = A, T, C or G
US-09-931-381A-15

Query Match 16.6%; Score 180; DB 4; Length 1689;
Best Local Similarity 54.0%; Pred. No. 7e-47;
Matches 444; Conservative 0; Mismatches 360; Indels 18; Gaps 3;

Qy 110 CCCAGCAGGTGCTGCACTTCTGTCGCGGCTGTTTGGGTGCTCTTGGACAACGTCG 169
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Qy 701 GGGAGAGACAGTACGACCTCCACAAGCCGCTCTTCTGTCATTAACGGGCGTGTCTCTTTGA 760
Db 872 GTAAAAAAGTACAAAGGCCATCCGGCTCATTTTGTCTATCATGCGGCTGTTTTTCATTT 931
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Db 992 ATGACTGTGAGCGGACGAAAGCATCTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
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Db 1052 ACTCCCACTGCTGATGAAACCCCGGTGATCTACGCTTTGTG 1093
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Job time : 212.112 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 09:53:05 ; Search time 755.748 Seconds
(without alignments)
8895.522 Million cell updates/sec

Title: US-10-623-472-32
Perfect score: 1083
Sequence: 1 atggataactacacagtggc.....aaaggcaggataataataa 1083

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	423.2	39.1	1776	21	US-10-741-600-13
4	423.2	39.1	14341	21	US-10-741-600-17557
5	422	39.0	1140	16	US-10-029-586-22780
6	422	39.0	1475	15	US-10-223-085-15
7	422	39.0	1475	15	US-10-223-084-15

8	422	39.0	1475	15	US-10-223-088-15
9	422	39.0	1475	15	US-10-223-090-15
10	422	39.0	1475	15	US-10-223-087-15
11	422	39.0	1475	15	US-10-223-083-15
12	422	39.0	1475	15	US-10-223-089-15
13	422	39.0	1475	16	US-10-223-081-15
14	422	39.0	1475	16	US-10-223-082-15
15	422	39.0	1475	17	US-10-305-654-15
16	422	39.0	1475	18	US-10-081-056-15
17	422	39.0	1645	15	US-10-225-567A-353
18	422	39.0	1698	19	US-10-717-597-300
19	422	39.0	143068	9	US-09-967-768A-316
20	422	39.0	143068	21	US-10-843-641A-6461
21	421.6	38.9	1270	17	US-10-305-720-756
22	421.2	38.9	1316	15	US-10-095-876A-3
23	420.4	38.8	1547	14	US-10-039-659-11
24	420.4	38.8	1547	19	US-10-754-071-11
25	420.4	38.8	1547	21	US-10-759-860-11
26	412.4	38.1	1035	18	US-10-623-472-31
27	412	38.0	1251	20	US-10-349-528-5
28	398.4	36.8	1050	9	US-09-912-025-1
29	237.8	22.0	7644	15	US-10-311-455-857
30	236	21.8	588	14	US-10-052-283-88
31	218.8	20.2	7644	15	US-10-311-455-858
32	184.8	17.1	1059	13	US-10-106-623-19
33	184.8	17.1	1059	20	US-10-772-037-19
34	183.2	16.9	1065	9	US-09-922-895-2
35	183.2	16.9	1065	21	US-10-767-521-2
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38	183.2	16.9	1071	22	US-10-988-267-21
39	183.2	16.9	1193	22	US-10-283-028-3
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45	183.2	16.9	1717	18	US-10-641-643-959

ALIGNMENTS

RESULT 1

US-10-623-472-32
; Sequence 32, Application US/10623472
; Publication No. US20040096913A1
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Groningen
; APPLICANT: Boddeke, Erik H.W.G.M.
; APPLICANT: Biber, Knut
; TITLE OF INVENTION: Cloning and expression of a new MCP receptor in glial cells
; FILE REFERENCE: 2183-6042US
; CURRENT APPLICATION NUMBER: US/10/623,472
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/NL02/00039
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: EP 01200181.4
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1083)
; OTHER INFORMATION: mCCR12 chemokine receptor sequence
US-10-623-472-32

Query Match 100.0%; Score 1083; DB 18; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;

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Db 241 CTTTCAAACCTGTGTTTCCCTGCTTCCCTCGCGTTCCTGGGCCCATACTGACGACACGCGG 300
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Db 1081 TAA 1083
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RESULT 2
US-10-741-600-12
; Sequence 12, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-12
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Query Match 39.1%; Score 423.2; DB 21; Length 1646;

Best Local Similarity 65.2%; Pred. No. 1.5e-131; Indels 33; Gaps 5;

Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;

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Db 202 ATGGCCAATTCACGCTGGCACCAGAGGATGAATATGATGTCC--TCATAGAAGGTGAA 258
QY 61 CTGGACAAACAGTGGCGGACCAAGTT-----CCGGCCCCGAGTTCCTCTCCCCCAG 114
Db 259 CTGGAGAGCGATGAGGACAGAGCAATGTGACAAGTATGACGCCAGGACACTCTCAGCCCCAG 318
QY 115 CAGGTCTCGAGTTCGTGCGCGGTGTTTGGGTGGTCTCTTGGACCAACGTCGTGGCG 174
Db 319 CTGTGCCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGCTCTGACCAATCTCTTGGTT 378
QY 175 GTGTTTATCTTGTGTAATAACAAGGACTCAAGAAATCTGGGGAACATCTACTTCTTAAAC 234
Db 379 GTGCTTATCTGTGTAAATATAAAGGACTCAACGCGTGGAAATATCTATCTTCTTAAAC 438
QY 235 CTGGCACTTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCCTGGGCCCATCTACTCAGCA 294
Db 439 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCTGCTTCTGGGCTCATGCTG----- 493
QY 295 CACGGGGAAGCCCTCGCAACGGGACCTGTAAAGTTCCTTGTGCGACTCCCACTCTCGGGC 354
Db 494 -----RKGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTTGGC 540
QY 355 TTATACAGCGAGGTGTTTTCCTCAACATCTCTCTCTTGTGCAAGGATACAGGGTGTGTTTC 414
Db 541 CTGTACAGTGAGACAATTTTCAATTGCTTCTGACTGTGCAAGGTACCTTAGTGTGTTTG 600
QY 415 CAAAGGGGAC---TGGGCTCCATCTTCAACAGACTGTCTGTGGTATTTGTTGGTGCATC 471
Db 601 CACAAGGGMAACTTTTCTCAGCCAGGAGGAGTGCCTCTGTGGCATCATTTACAAGGTGC 660
QY 472 CTGGCATGGCCATGCTGCTCTCTTTCCTGGAGTCTGTGTTTATGAGCCTCGG 531
Db 661 CTGGCATGGTAAACAGCCATCTTGGCCACTTTCCTGCAATTCCTGCTGATTCATTAACCTCAG 720
QY 532 ATGGAAGAGCAGAAACACAGTGTGCTTTTGGCAACCTCACTTCTTGGCAATGGAAGCG 591
Db 721 ATGGAAGACCAGAAATACAAAGTGTGCATTTTAGCAGAACTCCCTTCTCTGCCAGCTGATGAG 780
QY 592 CCCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGGTACTTGTCTTCTCTCTG 651
Db 781 ACATTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTGCGTCTTCTGCTCCCCCTA 840
```



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Qy 652 CTGGTGTATTAATCTGCTGAGGCAACTGAGGAGAGCAGAGCTTCAGGGAGAGACAG 711
Db 841 TTTATTTTTTACATTTCTATGTGCARATGAGAAAAACACTAAGGTTTCAGGGAGAGAGG 900
Qy 712 TACGACCTCCACAAGCGGCTCTGTGATACAGGGCGGTTCCTTTTGATGTGGCGCT 771
Db 901 TATAGCCCTTTTCAAGCTTGTGTTTGGCCRTAATGAGTGTCTTCTTCTGATGTGGCGGCC 960
Qy 772 TACAACACTGTGCTTTTCTGCTGCTTTTCCAGGAACACTTGTCCCTCGAGATGAGAG 831
Db 961 TACAATATTGATTTTCTGCTGCTTTTCAAGGAACACTTCTCCCTGAGTGTGAG 1020
Qy 832 AGCAGCTACACCTGGAGCGAAGTGTTCAGGTCAACAGTGTGAGCAACCACTGCG 891
Db 1021 AGCAGCTACAATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCACTGCG 1080
Qy 892 TGGCTCAACCGCTGCTCTATTGCTTCTTCCAGGAGGCTTTATGAGATCTTCCG 951
Db 1081 TGCATCAACCTCTCTCTGTATGCGTTCCTTGTATGGGA---CATTTAGCAATACCTCTGC 1137
Qy 952 AGCCTGTTCCCAACCGTGAATGATATCCCTTATCAAGTAGTGGAGGCTATCAGCAAGCG 1011
Db 1138 CGCTGTTTCCATCTGCGTAGTAACACCCACTTCAACCCAGGGGCGAGTCTGCACAGGC 1197
Qy 1012 CCTCCAAGGGAAGTTCATGGCAGGCCCATTTGAACCTGTACAGCAATTTGATCAAAAGGCG 1071
Db 1198 ACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAATGCAA 1257
Qy 1072 GA 1073
Db 1258 GA 1259
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RESULT 3

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US-10-741-600-13
; Sequence 13, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-13
```

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Query Match 39.1%; Score 423.2; DB 21; Length 1776;
Best Local Similarity 65.2%; Pred. No. 1.5e-131;
Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;

Qy 1 ATGGATACTACAGTGGCCCGGACCAAGTT-----CGGCGCCCGAGTTCCTCTCCCGCCAG 114
Db 328 ATGGCAATTRACGCTGGCACGAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGCCCGAG 444
Qy 61 CTGGACAACAGTGGCGCGGACCAAGTT-----CGGCGCCCGAGTTCCTCTCCCGCCAG 114
Db 385 CTGGAGAGCGATGAGGACGAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGCCCGAG 444
Qy 115 CAGGTGCTGACAGTTCGTGCGCGGTGTTTGGGTGCGTCTCTTGGACAAAGTGTGCGG 174
Db 445 CTGTGCGCATCACTCTGCTGCTGTGTTTGTGATCGGTGTCCTGGACAATCTCTCGTT 504
Qy 175 GTGTTTATCTTGGTGAATACAAAGGACTCAAGATCTGGGGAACATCTACTTCTTAAC 234
Db 505 GTGCTTATCTCGGTGAATATAAAGGACTCAACCGGTGGAAATATCTATCTCTTAAC 564
Qy 235 CTGGCACTTTCAAAACCTGTGTTTCTGCTTCCCTGCGGCTTCTGGGCGCCATCTGCGAGCA 294
```

```
Db 565 TTGGCAGTTTCTAATCTGTTTCTTGCTTACCCTGCCCCTTCTGGGCTCATGCTG----- 619
Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGGACTCCACTCTCGGCG 354
Db 620 -----RGGCGATCCCATGTGTAAAAATTTCTCATTTGGAAGTCTTCTGTTGGC 666
Qy 355 TTATACAGCGAGTGTGTTTCCAAACATCTCTCTCTGTCGCAAGGATACAGAGTGTGTTTCC 414
Db 667 CTGTACAGTGAACATTTTCAAATGTCCTCTGACTGTGCAAGGATACCTAGTGTGTTTGG 726
Qy 415 CAAGGGGAC---TGGGCTCCATCTTACGACAGTGTCTTGTGTTGTTGCTGCGTCATC 471
Db 727 CACAAGGGAACATTTTCTCAGCCAGGAGGAGGCTGCTGTGGCATCATTTACAAGTGTG 786
Qy 472 CTGCGATGGGCGATGGGCTACTGCGCTCTCTTTGCGCGAGTCTGTGTTTATATGAGCTCGG 531
Db 787 CTGCGATGGGTAAACAGCATTTCTGCGCACTTTGCTGATWCRIGGTTTATAACCTCAG 846
Qy 532 ATGGAAGACAGAAACAAAGTGTGCTTTGGCAAACTCTCTTTCGCCAATCGAAGCG 591
Db 847 ATGGAAGACAGAAATACAAAGTGTGCTTTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 906
Qy 592 CGGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTTGTCTTCTCTG 651
Db 907 ACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCCGTTCTTGTCTCTCCCTTA 966
Qy 652 CTGCTGTTTAAATCTGCTGCGAGCAACTGAGGAGAGGAGAGCTTCAGGGAGAGACAG 711
Db 967 TTTATTTTATCATTTCTCTATGCGAATATGAGAAACACTAAGGTTTCAGGGAGCAGAGG 1026
Qy 712 TACGACCTCCACAAGCGGCTCTTGTATACACGGCGTGTTCCTTTTGTATGCGCGCT 771
Db 1027 TATAGCCTTTTCAAGCTTGTGTTTGGCCRTAATGTTAGTGTCTTCTCTGATGTGGCGGCC 1086
Qy 772 TACAACACTGTGCTTTTCTGCTGCTTTCAGGAACACTTGTCCCTCAGGATGAGAG 831
Db 1087 TACAATATTGCAATTTTCTGCTCCACTTTCAAGAAACACTTCTCCCTGAGTGAAGTGAAG 1146
Qy 832 AGCAGCTACCACTGGAGCGCAAGTGTTCAGGTCAACAGCTGTTAGCAGCACCACTGCG 891
Db 1147 AGCAGCTACCACTGGAGCAAAAGTGTTCATCATCACTAACTATCGCCACCACTGCG 1206
Qy 892 TGCCTCAACCGCTGCTCTATTGCTTCTTTCAGCGGAAGGCTTTTATGAGATACCTTCCG 951
Db 1207 TGATCAACCTCTCTGATGCGTTCCTGATGCGA---CATTTAGCAATATCTCTGCG 1263
Qy 952 AGCCTGTTCCCAACCGTGAATGATATCCCTTATCAAGTAGTGGAGGCTATCAGCAAGG 1011
Db 1264 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTTCAACCCAGGGGCGAGTCTGCAACAGG 1323
Qy 1012 CTTCAAGGGAAGTTCATGCGAGGCCCATTTGAACTGTACAGCAATTTTCATCAAAAGGAG 1071
Db 1324 ACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAATGCA 1383
Qy 1072 GA 1073
Db 1384 GA 1385
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RESULT 4

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US-10-741-600-17557
; Sequence 17557, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 17557
; LENGTH: 14341
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17557

Query Match      39.1%; Score 423.2; DB 21; Length 14341;
Best Local Similarity 65.4%; Pred. No. 4.6e-131;
Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATGATCTCTTAATCTTAGACGACTAC 60
Db 6892 ATGCCCAATTCACAGCTGGCCACGAGGATGATATGATGTC---TCATAGAAGGTGAA 6948
QY 61 CTGGACAACAGTGGCGGACCAAGTT-----CCGGCCCCCGAGTTCTCTCCCCCAG 114
Db 6949 CTGGAGAGCATGAGGACAGCAATGTGACAAGTATGACGCCCGAGCACTCTCAGCCAG 7008
QY 115 CAGGTCTGCAGTCTGCTCGCGGGTGTGCGGTGGTCTCTTGACACAGTCTGGCG 174
Db 7009 CTGGTGCATCACTCTGCTCTGCTGTGTGTGTGATCGGTCTCTGACCAATCTCCCTGGTT 7068
QY 175 GTGTTTATCTTGTGAAATACAAAGGACTCAAGAACTCTGGGAACATCTACTTCTTAAC 234
Db 7069 GTGCTTATCTGTAAATATAAGGACTCAAGCGGTGGAAATATCTATCTCTTAAC 7128
QY 235 CTGGCACTTTCAAACTGTGTTCTGCTTCCCTGCGGTCTGGGCCCATATCTGACGA 294
Db 7129 TTGGCAGTTTCTAACTGTGTTCTGCTTACCTGCGCTTCTGGGCTCATGCTG---- 7183
QY 295 CACGGGGAAAGCCCTGGCAGGGAGCTGTAAAGTTCTTGTGGACTCCCACTCTCGGCG 354
Db 7184 -----RKGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGCG 7230
QY 355 TTATACAGCAGGTGTTTTCCAACTCTCTCTGTGCAAGATACAGGTTGTTTTCC 414
Db 7231 CTGTACAGTGAGACATTTTTCAATTCCTCTGACTGTGCAAGGTACCTAGTGTGTTG 7290
QY 415 CAAGGGGGAC---TGGCTCCATCTTCAACAGAGTGTCTGTTGGTATGTTGGTGATC 471
Db 7291 CACAAGGGMAACTTTTTCTCAGCAGGAGGAGGTGCTCTGTGGCATCATTAAGTGTG 7350
QY 472 CTGGCATGGCCATGCTACTGCTGCTCTCTTCCCGAGTCTGTGTTTATGAGCTCGG 531
Db 7351 CTGGCATGGGTAAACAGCCATCTGGCCACTTTCGCTGAATGCTGTGTTTATAAACCTCAG 7410
QY 532 ATGGAAGACAGAAACACAGTGTGCTTTGGCAAACTCCTCCTCTTGCCAAATCGAAGCG 591
Db 7411 ATGGAAGACCAAGATACAGTGTGATTTAGCAGAACTCCCTTCTGCGAGCTGATGAG 7470
QY 592 CCCTCTGGAAGTACGTTCTGAGCTCAAAATGATCATCTTGTTGTTCTGTTTCTCTG 651
Db 7471 ACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTTCGGTTCTTCTCTCCCTTA 7530
QY 652 CTGGTTTTTATATCTGCTGACGCAACTGAGGAGAGGACAGAGTTCAGGGAGAGACAG 711
Db 7531 TTTATTTTACATTTCTATGTGCAATGAGAAAACATAAGTTTCAGGGAGAGAGG 7590
QY 712 TAGGACTCTCAAGCGGGCTCTGTATACAGGGGGTGTTCCTTTTGTATGTTGGGGCCT 771
Db 7591 TATAGCCTTTTCAAGCTTGTGTTTGGCCTAATGTTAGTCTTCTCTGATGTTGGGGCCC 7650
QY 772 TACAACATGTGCTTTTCTGCTGCTTTCCAGGAACACTTGTCTCTGAGGATGAGAG 831
Db 7651 TACAATATTGCAATTTTCTGCTCACTTTTCAAGAAACACTTCTCTGAGTGAAGTCAAG 7710
QY 832 AGCAGCTACCACTGGACGCAAGTGTTCAGGTACACAGCTGTTAGCGACCACTGTC 891
Db 7711 AGCAGCTACCACTGGACAAAAGTGTTCATCATCTAACTCATCGCACCACTGTC 7770
QY 892 TGGCTCAACCCGCTGCTCTATTGTTCTTGTACCGGAAGCCCTTTATGAGATACCTTCGC 951
Db 7771 TGCAATCAACCCCTCTCTGTTATGCTTTCTTGTATGGGA---CATTTAGCAAAATACCTCTGC 7827
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QY 952 AGCCTTTTCCACAGGTGCAATGATATCCCTATCAAAGTAGTGGAGGCTATCAGCAGCG 1011
Db 7828 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGAGTCTGCACAGGC 7887
QY 1012 CTCCCAAGGGAAGGTCTATGGCAGGCCCAATTGAAGTGTACAGCAATTTGCAATCAAAGCAG 1071
Db 7888 ACATCGAGGGAAGAACCTGACCATTTCCACGGAAGTGTAAACTAGCATCCACCAATGCAA 7947
QY 1072 GA 1073
Db 7948 GA 7949

RESULT 5
US-10-029-386-22780
; Sequence 22780, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22780
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO U95626.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EST HUMAN HIT: B1834559.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O97883, EVALUE 2.00e-63
; OTHER INFORMATION: NT HIT: g114736672, EVALUE 0.00e+00
US-10-029-386-22780

Query Match      39.0%; Score 422; DB 16; Length 1140;
Best Local Similarity 65.5%; Pred. No. 3.1e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCGGACGATGAATGATGTCCTTAATCTTAGACGACTAC 60
Db 13 ATGGCCAATTAACACGCTGGCACCAAGAGTGAATATGATGTCC---TCATAGAAGGTGAA 69
QY 61 CTGGACAACAGTGGGGCCGACCAAGTT-----CCGGCCCCCGAGTTCTCTCCCCCAG 114
Db 70 CTGGAGAGCATGAGGACAGCAATGTGACAAGTATGACGCCCGAGCACTCTCAGCCAG 129
QY 115 CAGGTCTGCAGTCTGCTGCGGGTGTGCGGTGGTCTCTTGGACAAACGTTGCTGGCG 174
Db 130 CTGGTGCCATCACTCTGCTCTGCTGTGTGTGTGTGATCGGTGCTCTGACAAATCTCTGTT 189
QY 175 GTGTTTATCTTGGTGAATACAAAGACCTCAAGAACTCTGGGGAACATCTACTTCTTAAAC 234
Db 190 GTGCTTATCTGTGTAATAATATAAGGACTCAACCGGTGGAATAATCTATCTTCTTAAAC 249
QY 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTCTCTGGGCCCATACTGACGA 294
Db 250 TTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCGCTTCTGGGCTCATGCTG---- 304
QY 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCCACTCTCTCGGC 354
Db 305 -----GGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGC 351
```

355 TTATACAGCGAGGTGTTTCCAAATCCTCTCTGTGCAAGGATACAGGGTGTTC 414
352 CTGTACAGTGAACATTTTCAATGTCCTTCTGACTGTGCAAGTACTAGTGTTC 411
415 CAAGGGCGAC---TGGCCTCCATCTTACAGACAGTGTCTTGGGATTTGTCGTGCATC 471
412 CACAAGGCAACATTTTCTCAGCCAGGAGGAGGTCCTCTGGCATCATTTACAAGTGC 471
472 CTGGCATGGGCATGGCTACTCGCTCTCTTTGCCGAGTCTGTGTTTATGAGCCTGG 531
472 CTGGCATGGGTAAACGCAATCTGCGCACTTCTGCTGAATAGTGGTTTATACCTCAG 531
532 ATGGAAGACAGAAACACAACTGTGCTTTGGCAACCTCACTCTTGCCCAATCGAAGCG 591
532 ATGGAAGACAGAAATACAAGTGTGCATTTAGCAGAACTCCCTCTGCCAGCTGATGAG 591
592 CCGCTCTGGAGTACGTTCTGACGTCRAAATGATCATCTTGGTACTTCTTCTCTG 651
592 ACATTCTGGAAGCATTTTCTGACTTTAAATGAATGAACATTTCCGTTCTTCTCCCTCA 651
652 CTGGTTTATTAATCTGCTGCAGGCACTGAGGAGAGGAGGCTTCAGGGAGAGACAG 711
652 TTTATTTTACATTTCTCTATGTGCAATGAGAAACACTAAGTTTCAGGAGCAGAGG 711
712 TACGACCTTCCAAAGCGGCTCTTGTCTATACCGGCGTGTCTTCTTTGATGTGGCGCT 771
712 TATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTGATGTGGGCGCC 771
772 TACAACACTGTCTTCTCTGCTGCTTTCAGGAACTCTTCTGCTGCGAGGATGAGAG 831
772 TACAATATTCATTTTCTCTGCTGCACTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAG 831
832 AGCAGCTACCACTGGAGCGAAGTGTTCAGGTTCACACAGCTGTAGCGACCACTGC 891
832 AGCAGCTACAATCTGGAACAAAGTGTTCACATCACTAACTATCGCCACCACTGC 891
892 TGCCTCAACCGCTGCTCTATTGCTTCTTGACCGGAGGCTTTATGAGATACCTTCGC 951
892 TGCATCAACCTCTCTCTGATGCGTTTCTTGATGGA---CATTTAGCAATACCTCTGC 948
952 AGCTGTTCACCGTGAATGATATCCCTATCAAGTAGTGGAGGCTATCAGCAAGC 1011
949 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGC 1008
1012 CCTCAAGGGAAGTCAATGCGAGGCCCACTGAACTGTACAGCAATTTGATCAAAAGGCAG 1071
1009 ACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCACCAATGUA 1068
1072 GA 1073
1069 GA 1070

RESULT 6

US-10-223-085-15
Sequence 15, Application US/10223085
Publication No. US20030100497A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Masters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P223P1C10
CURRENT APPLICATION NUMBER: US/10/223,085
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo sapiens
US-10-223-085-15

Query Match 39.0%; Score 422; DB 15; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGAATACTACACAGTGGCCCCCGACGATGATGATGCTTAATCTTAGACGACTAC 60
Db 29 ATGSCCAATTACAGCTGCGCACGAGAGATGATGATGCTCC---TCATAGAAGTGAA 85
Qy 61 CTGGAACAAGTGGCGCGGACCAAGTT-----CGGCGCCCGAGTTCTCTCCCCCAG 114
Db 86 CTGAGAGCGATGAGGAGAGCAATGTGCAAGATGACGCCCGAGGCACTCTCAGCCAG 145
Qy 115 CAGTGTCTCAGTTCTCTCGCGGTGTTGCGGTGGTCTCTTGGACAACGTCGTGCGG 174
Db 146 CTGCTGCCATCCTCTCTCTGCTGTTGTGATCGGTGCTCTGGAACAATCTCTCTGTT 205
Qy 175 GTGTTATCTTGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAC 234
Db 206 GTGCTTATCTGTAAATATAAAGGACTCAACGCGTGGAAATATCTATCTTAAC 265
Qy 235 CTGGCACTTTCAAACTGTGTTTCTCTCTCTCTCTGCGGTCTGCGGCCCATCTGACGA 294
Db 266 TTGGCAGTTTCTAACTTGTGTTTCTGCTTACCTGCGCTTCTGCGGTCTAGCTG- 320
Qy 295 CAGGGGAAGCCCTGGCAAGGAGCTGTAAAGTCTTGTGCGACTCCACTCTCGGCG 354
Db 321 -----GGGCGGATCCCATGTGTAAATATCTCATTTGAGTGTACTTCTGTTGG 367
Qy 355 TTATACAGCGAGTGTGTTTCCAAACATCTCTCTCTCTGTCGAAGGATACAGGGTGTTC 414
Db 368 CTGTACAGTGAACATTTTCAATTTGCTTCTGACTGTGCAAGGATACCTAGTGTTC 427
Qy 415 CAAGGGCGAC---TGGCCTCCATCTTCAAGACAGTGTCTGTGTGATTTGTCGTGCATC 471
Db 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTCCTGTGTCATCATTTACAAGTGC 487
Qy 472 CTGCGATGGGCCATGGCTACTGCGCTCTCTTGGCCGAGTCTGTGTTTATGAGCTCGG 531
Db 488 CTGCGATGGGTAAACAGCCATTTCTGGCCACTTTCTGCTGAATACAGTGGTTTATAAACCTCAG 547

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QY 532 ATGGAAGACAGAAACACAAGTGTGCTTTGGCAACCTCACTTCTTGCCAAATCGAAGCG 591
|||
Db 548 ATGGAAGACAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
|||
QY 592 CCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGTGTTGCTTTCTCTCTG 651
|||
Db 608 ACATTCTGGAAGCATTTCTGACTTTAAAATGACATTTGGTCTTGTCTCTCCCTCA 667
|||
QY 652 CTGGTTTTTAATCTGCTCGAGCAACTGAGGAGAGGAGAGCTTTCAGGGAGAGACAG 711
|||
Db 668 TTTATTTTTCATTTCTCTATGTGCAATGAGAAAAACATAAGGTTTCAGGGAGAGAGG 727
|||
QY 712 TACGACTCCACAAGCGGCTCTTGTCAATACGCGGTGTTCTTTTGTGTCGGGCGCT 771
|||
Db 728 TATAGCCTTTTCAAGCTTGTTTTGGCATAATGTGTCTTCTCTGTGATGTGGGCGCC 787
|||
QY 772 TACAACACTGTGCTTTTCTGTCTGTCTTCCAGGAACACTTGTCCCTGCGAGGATGAGAAG 831
|||
Db 788 TACAATATTCATTTTCTGTCTCCACTTTCAAGAACACTTCTCCCTGAGTGACTGCAAG 847
|||
QY 832 AGAGCTTACCCTGGAGCGCAAGTGTTCAGGTCAACAGCTGGTAGGACCAACCCACTGC 891
|||
Db 848 AGAGCTTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACTGC 907
|||
QY 892 TGGCTCAACCGCTGCTCTATTTGCTTCTTGACCGGAAGGCTTTATGAGATACCTTCGC 951
|||
Db 908 TGCATCAACCTCTCTCTGTATGCGTTTCTTGTATGGGA---CATTTAGCAATACCTTCGC 964
|||
QY 952 AGCTGTCTCCAGCGGTGCAATGATATCCCTTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
|||
Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC 1024
|||
QY 1012 CTCCAAAGGAAGTCAATGGAGGCCCAATTGAATGTAAGCAATTTGCAATCAAAAGGCGAG 1071
|||
Db 1025 ACATCGAGGAAGAACCTGACCACTTCCACCGAAGTGTAAACTAGCATCCCAAAATGCAG 1084
|||
QY 1072 GA 1073
||
Db 1085 GA 1086
||
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RESULT 7

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US-10-223-084-15
; Sequence 15, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3235P15
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-084-15
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Query Match 39.0%; Score 422; DB 15; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAAATTACACAGTGGCCCGGACGATGATATGATGTCTTAATCTTAGACGACTAC 60
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Db 29 ATGGCAATTTACACGCTGGCACCGAGGATGATATGATGTCC---TCATAGAAGGTGAA 85
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QY 61 CTGGACAAACAGTGGGCGGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCAG 114
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Db 86 CTGGAGAGCGATGAGGACGAGCAGCNAATCTGACAGTATGACGCCCGAGCACTCTCAGCCCAG 145
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QY 115 CAGGTCTGCAAGTTCTGTCGCGGTGTTTGGCGGTGTTCTTTGGACAAACAGTGTGCGCG 174
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Db 146 CTGGTCCCATCACTCTGCTCTGCTGTGTGTGTGATCGGTGTCCTGGACAAATCTCTCGT 205
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QY 175 GTGTTTATCTTGGTGAATACAAAGGACCTCAAGAACTCGGGAACTACTTCTCTAAAC 234
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Db 206 GTGCTTATCTGGTAAATATAAAGGACTCAACCGGTGGAATAATCTATCTCTTAAC 265
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QY 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTGGGCCCACTACTGCAGCA 294
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Db 266 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCTGCGCTTCTGGGCTCATGCTG--- 320
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QY 295 CACGGGGAAGCCCTCGGCAACGGGACCTGTAAAGTCTTGTGCGGACTCCTCTCTCGGGC 354
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QY 355 TTATACAGCGAGGTGTTTCTCAACATCTCTCTTGTGCAAGGATACAGGGTGTGTTTCC 414
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Db 368 CTGTACAGTGAACATTTTTTCAATTCCTTCTGACGTGCAAGGTACCTAGTGTGTTTGG 427
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QY 415 CAAGGCGGAC---TGGCCTCCCATCTTTACGACAGTGTCTTGTGGTATTTGTTGGCGTCA 471
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Db 428 CACAAGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTAACAAGTGTG 487
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QY 472 CTGGCATGGGCCATGCGCTACTGCGCTCTTTTGGCCGAGTCTGTGTTTATGAGCTCGG 531
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QY 532 ATGGAAGACAGAAACACAAGTGTGCTTTTGGCAAACTCACTTCTTGCCAAATCGAAGCG 591
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Db 548 ATGGAAGACAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
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QY 592 CCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGTGTTGCTTTCTCTCTG 651
|||
Db 608 ACATTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTTCGGTCTTGTCTCTCCCTCA 667
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QY 652 CTGGTTTTTAATCTGCTGCGGCAACTGAGGAGAGGAGGAGCTTTCAGGGAGAGACAG 711
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Db 668 TTTATTTTTCATTTCTCTATGTGCAAAATGAGAAAAACACTAAGTTCAGGGAGAGAGG 727
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Qy	712	TACGACCTCCACAAGCGCGCTCTTGTGCATAAAGCGCGCTGTTCTCTTTTGATGTGGCGCCCT	771
Db	728	TATAGCCCTTTTCAAGCTGTGTTTTGGCCATAATGGTAGTCTCTCTCTGATGTGGCGGCC	787
Qy	772	TACAACACTGTGCTTTTCTGCTGCTTTCCAGGAAACACTTGTCTCCCTGCAGGATGAGAAG	831
Db	788	TACAAATATGTGATTTTCTCTGTCACATTTTCAAGAACAACCTTCTCCCTGAGTGACTGCAAG	847
Qy	832	AGCAGCTACCACTCGGACGCAAGTGTTTCAGGTCCACAGCTGGTAGCGAACCCACCCTGCG	891
Db	848	AGCAGCTACAATCTGGACAAAGTGTTCCACATCACTAACTCATCGCCACCACCACCTGCG	907
Qy	892	TGCGCTCAACCGCTGCTCTATTTCGTTCTTGACCGGAAGGCTTTATGAGATACCTTCGC	951
Db	908	TGCATCAACCCCTCTCTGTATGCGTTTTCTTGATGGGA---CATTTAGCAAAATACCTCTGCG	964
Qy	952	AGCCTGTTTCCACAGGTGCAATGATATCCCTATCAAAGTAGTGAGGCGTATCAGCAAGCG	1011
Db	965	CGCTGTTTCCATCTGCGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC	1024
Qy	1012	CCTCCAAGGGAAGTTCATGGCAGCGCCCATTTGAACCTGTACAGCAATTTGGCATCAAAGGCAG	1071
Db	1025	ACATCGAGGGAAGAACCTGACCACTTCCACCGAAGTGTAAACTACCATCCACCAATGCAG	1084
Qy	1072	GA	1073
Db	1085	GA	1086

RESULT 8

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US-10-223-088-15
; Sequence 15, Application US/10223088
; Publication No. US20030105012A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C6
CURRENT APPLICATION NUMBER: US/10/223,088
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328

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QY 892 TGCGTCAACCGGTGCTCTATTGTTCTTCTTGACGGAGGCGCTTATGAGATACCTTCGC 951
DB 908 TGCATCAACCTCTCTGTATGCGTTCTTGTATGGGA---CATTTAGCAAAATACCTCTGC 964
QY 952 AGCTGTGTTCCAGCGGTGCAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
DB 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCAGGGGCGAGTCTGCACAAGGC 1024
QY 1012 CTCCAAAGGAAGGTCTAGCAGGCGCCCATTTGAATCTGTACAGCAATTTGCAATCAAAAGGCGAG 1071
DB 1025 ACATCGAGGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCCAACCAATGCAA 1084
QY 1072 GA 1073
DB 1085 GA 1086

RESULT 9

US-10-223-090-15
; Sequence 15, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F235P1C2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-090-15

Query Match 39.0%; Score 422; DB 15; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCCGGACGATGAATATATGATGCTTAATCTTAGACGACTAC 60
DB 29 ATGGCCAATTACACGCTGGCACGAGGATGAATATGATGTC---TCATAGAGGTGAA 85
QY 61 CTGGCAACAGTGGGGCCGGACCAAGTT-----CGGGCCCCGAGTTCCTCTCCCCCAG 114
DB 86 CTGGAGAGCGATGAGGACAGACGCAATGTGACAGTATGACGCCGAGCACTCTCAGGCCAG 145
QY 115 CAGGTCTCGAGTTCGTCTGCGCGGTGTTTGGGTGGGTCTCTTGGACAACAGTGTCTGGCG 174
DB 146 CTGGTCCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGACAATCTCTCTGGTT 205
QY 175 GTGTTTATCTTGTGTAATACAAAGGACTCAAGAAATCTGGGGAACATCTACTTCTTAAAC 234
DB 206 GTGCTTATCTGTGTAATAATATAAGGACTCAACGGGTGAAATATCTATCTTCTTAAAC 265
QY 235 CTGGCACTTTCAAAACCTGTGTTTCTGTCTTCCCTGCGGTTCTGGGCCCATACTATGCAGCA 294
DB 266 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCCTGCCCCCTCTTGGGCTCATGCTG---- 320
QY 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGTGGACTCACACTCCTCGGGC 354
DB 321 -----GGGGCGATCCCATGTGTAAAAATCTCATTTGGACTGTACTTTCGTGGGC 367
QY 355 TTATACAGCGAGTGTGTTTCTCAACATCTCTCTTGTGCAAGGATACAGGGTGTGTTTCC 414
DB 368 CTGTACAGTGAACATTTTCAATTCCTTCTGACTGTGCAAGGTACTCTAGTGTGTTTGG 427
QY 415 CAAGGGCGAC---TGSCCTCCATCTTTCACGACAGTGTCTTGTGTGTTATGTTGCGTGCATC 471
DB 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTAACAAGTGC 487
QY 472 CTGGCATGGGCATGGCTACTGGCTCTCTTTCGCCGAGTCTGTGTTTATGAGCTCGG 531
DB 488 CTGGCATGGGTAAACAGCCACTTCTGGCCACTTTCGCTGAATACGTGGTTTATAAACCTCAG 547
QY 532 ATGGAAGACAGAAACACAAAGTGTGCTTTTGGCAACCTCACTTCTTGCCAAATCGAAGCG 591
DB 548 ATGGAAGACAGAAATACAAAGTGTGATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
QY 592 CGCTCTGGAAGTACGTTCTGACGTCAAAAATGATCATCTTGGTACTTGTCTTCTCTCTG 651
DB 608 ACATTCTGGAAGCATTTTCTGACTTTTAAAAATGAAACATTTTCGGTTCTTCTCTCCCCCTA 667
QY 652 CTGGTTTTTATATCTGCTGCAAGGAACTGAGGAGAGCAGAGCTTTCAGGAGAGACAG 711
DB 668 TTTATTTTACATTTCTCTATGTGCAAAATGAGAAAAACAATAAGGTTTCAGGGAGCAGAGG 727
QY 712 TAGGACCTCCAAAGCGGCTCTTGTCAATAACGGGGTGTCTTCTTTTGTATGTTGGGCGCCT 771
DB 728 TATAGCTTTTCAAGCTTGTGTTTGGCAATATGTTAGTCTTCTTCTGATGTGGGCGCCC 787
QY 772 TACAACACTGTCTTTTCTGCTGTCTGTTTCCAGGAACACTTGTCTCTGAGGATGAGAAG 831
DB 788 TACAATATTGCAATTTTCTGCTCCACTTTTCAAGAAACACTTCTCTCCTGAGTGAAGCAAG 847
QY 832 AGCAGCTACCACTGACGCAAGTGTTCAGGTCAACAGCTGGTAGGAGCACCACCTGCG 891
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QY 892 TGGCTCAACCCGCTGCTCTATTGCTTCTTGTAGCCGGAAGGCTTTTATGAGATACCTTCGC 951
DB 908 TGCATCAACCTCTCTCTGTATGCGTTTCTTGTATGGA---CATTTAGCAAAATACCTCTGC 964
QY 952 AGCTGTTTCCACGGGTGCAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
DB 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGC 1024
QY 1012 CTCCAAAGGGAAGTTCATGCGAGGCGCAATTGAACTGTACAGCAATTTGATCAAAAGCAG 1071
DB 1025 ACATCGAGGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCCAACCAATGCAA 1084

Qy 1072 GA 1073
Db 1085 GA 1086

RESULT 10

US-10-223-087-15

Sequence 15, Application US/10223087

Publication No. US20030109438A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P3235P1C4

CURRENT APPLICATION NUMBER: US/10/223,087

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 10/081,056

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/213,637

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/219,556

PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/220,624

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/220,664

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/222,695

PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: US 09/643,657

PRIOR FILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: PCT/US00/23522

PRIOR FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/230,978

PRIOR FILING DATE: 2000-09-07

PRIOR APPLICATION NUMBER: US 60/232,887

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 09/664,610

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US 60/242,922

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 09/709,238

PRIOR FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: PCT/US00/30952

PRIOR FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: PCT/US00/30873

PRIOR FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: US 09/747,259

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: PCT/US00/34956

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: US 09/767,609

PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
LENGTH: 1475
TYPE: DNA
ORGANISM: Homo sapiens
US-10-223-087-15

Query Match 39.0%; Score 422; DB 15; Length 1475;

Best Local Similarity 65.5%; Pred. No. 3.5e-131; Mismatches 340; Indels 33; Gaps 5;

Matches 709; Conservative 0;

Qy 1 ATGGATTAACACAGTGGCGCCCGGACGAGTGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 29 ATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCC---TCATAGAGGTGAA 85
Qy 61 CTGGACAACAGTGGCGCGGACCAAGTT-----CGGCGCCCGGAGTTCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGCAATGTGACAAGATGACGCCCGGCACTCTCAGCCAG 145
Qy 115 CAGGTGCTGCAGTTCTCTCGCGCGTGTTCGCGTGGTCTCTTGGACAAGTGTGTGCGG 174
Db 146 CTGGTGCACACTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 205
Qy 175 GTGTTTATCTTGGTGAATACAAAGGACTCAAGAACTCTGGGGAACATCTACTTCTTAAC 234
Db 206 GTGCTTATCTGTGTAATAATAAAGGACTCAACCGCTGGAAATATCTATCTTCTTAAC 265
Qy 235 CTGGCACTTTCAAACCTGTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
Db 266 TTGGCAGTTTCTAACTTGT 320
Qy 295 CACGGGGAAGCCCTGGCAAGCGGACCTGTAAAGTCTTGTGCGACTCCACTCTCTCGGGC 354
Db 321 -----GGGCGGATCCCATGTGTGTAAATTTCTCATTTGAGCTGTACTTGTGGGC 367
Qy 355 TTATACAGCGAGGTGTTTTCACACATCTCTCTCTGTGTGCAAGGATACAGGGTGTTC 414

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Db 368 CTGTACAGTGAGACATTTTCAATGCTCTCTGACTGTGCAAAAGGTACCTAGTGTGTTTG 427
Qy 415 CAAGGGCGAC---TGGGCTCCATCTTCACGACAGTGTCTTGTGTGTAATTTGTGGTGCATC 471
Db 428 CACAAGGGCACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTG 487
Qy 472 CTGGCATGGGCATGGCTACTCGGCTCTCTTTGGCCGAGTCTGTGTTTATGAGCCTCGG 531
Db 488 CTGGCATGGGTAAACAGCACTTCTGGCCACTTTGCCGTAATACGGTGGTTTATAAACCTCAG 547
Qy 532 ATGGAAGACAGAAACACAAGTGTGCCCTTTGGCAAACTCACTTCTTGCCAAATCGAAGCG 591
Db 548 ATGGAAGACAGAAATACAAGTGTGCATTTAGCAGAACTCCCTCTCGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTGTTTTCCTCTG 651
Db 608 ACATTTCTGGAAGCATTTCTGACTTTAAAAATGAACATTTTCGGTCTCTTGTCTCCGCCCTA 667
Qy 652 CTGGTTTTTATCTCTCGCAGGCACTGAGGAGAGGCGAGAGCTTCAGGGAGAGACAG 711
Db 668 TTTATTTTATCACTTCTCTATGTGCAAAATGAGAAAAACATAAGGTTTCAGGGAGCAGAG 727
Qy 712 TAGCACTCCACAGCCGGCTTTGTTCATTAACGGGGCTGTCTCTTTGATGTGGGGCCT 771
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Qy 832 AGCAGCTACCACTGGAGCGAAGTTTCAGGTTCAGTTCACAGCTGTGTAGGACCACTGTC 891
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Qy 892 TGGGTCAACCCGGCTGCTCTATTGCTTCTTGACCGGAAGCCCTTTATGATACCTTTCG 951
Db 908 TGATCAACCCCTCTCTGATGCGTTTCTTGATGGGA---CATTTAGCAATACCTTCTG 964
Qy 952 AGCTGTGTCCAGCGGTGCAATGATATCCCTATCAAAAGTATGAGGCTATCAGCAAGCG 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGG 1024
Qy 1012 CTCCAAAGGAAGTCAATGCGAGCCCATTTGACTGTACAGCAATTTGCATCAAGGCGAG 1071
Db 1025 ACATCGAGGAAGAACCTGACCATTCACCGAAAGTGTAAACTAGCATGCCAACCAATGCAA 1084
Qy 1072 GA 1073
Db 1085 GA 1086
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RESULT 11
US-10-223-083-15

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; Sequence 15, Application US/10223083
; Publication No. US2003011912A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
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; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

; FILE REFERENCE: P3235PIC8

; CURRENT APPLICATION NUMBER: US/10/223,083

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/213,637

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/219,556

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; PRIOR APPLICATION NUMBER: US 60/220,624

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; PRIOR APPLICATION NUMBER: US 60/220,664

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; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 09/643,657

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US00/23522

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 383

; SEQ ID NO 15

; LENGTH: 1475

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-223-083-15

Query Match 39.0%; Score 422; DB 15; Length 1475;

Best Local Similarity 65.5%; Pred. No. 3.5e-131;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGATACTACACAGTGGCCCGGACGATGAATATGATGTCTATCTTAGACGACTAC 60

Db 29 ATGGCCAAATACACGCTGGCACACAGGATGAATATGATGTCC---TCATAGAAGTGAA 85

Qy 61 CTGGCAACACAGTGGGCGGACCAAGTT-----CGGGCCCCGAGTTCCTCTCCCCCAG 114

Db 86 CTGGAGAGCGATGAGGACAGAGCAATGTACAAGTATGAGCCCGACGACTCTCAGCCAG 145

Qy 115 CAGGTGCTCGAGTTCGTGCGGGTGTGGGGTCTCTTGGACAAAGTGTCTGGCG 174

Db 146 CTGGTCCATCACTCTGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 205

Qy 175 GTGTTTATCTGTGAAATACAAAGGACTCAAGAAATCTGGGGAACATCTACTTCTTAAAC 234

Db 206 GTGCTTATCTGTGAAATATAAAGGACTCAAAACGGGTGGAATAATCTATCTTCTTAAAC 265

Qy 235 CTGGCACTTTCAAAACCTGTGTTTCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCT 294

Db 266 TTGGCAGTTCCTTAACTTGTGTTTCTTGTCTTACCTGCTTCCTGCTTCCTGCTTC 320

Qy 295 CAGGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCCTTGTGGACTCCTCCTCGGC 354

Db 321 -----GGGGCGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCGTGGGC 367

Qy 355 TTATACAGCGAGTGTGTTTTCACACATCTCTGCTTCCTGCTTCCTGCTTCCTGCTTC 414

Db 368 CTGTACAGTGAGACATTTTTCATTTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCT 427

Qy 415 CAAAGGCGAC---TGGCCTTCCATCTTTCAGCAGAGTGTCTTGTGGTATTTGTGCTGCATC 471

Db 428 CACAAGGGCACTTTTCTCAGCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 487

Qy 472 CTGGCATGGGCCATGGCTACTGCTCTCTTTGCGCGAGTCTGTGTTTATGAGCCTCGG 531

Db 488 CTGGCATGGGTAAACAGCCACTTCTGGCCACTTTTGGCCGAAATACGCTGCTTATAAACCTCAG 547

Qy 532 ATGGAAGACAGAAACACAAGTGTGCTTTTGGCAAACTCACTTCTTGTGCCAATCGAAGCG 591


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Db 548 ATGAAGACCAAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTAGTCTGACGTCAAAAATGATCATCTTGGTACTTGTCTTCTCTG 651
Db 608 ACATTTCTGGAAGCAATTTCTGACTTTAAAAATGAACATTTTCGGTCTTGTCTCTCCCTA 667
Qy 652 CTGGTTTTTATAATCTGCTGCGAGGCAACTGAGGAGAGAGAGAGCTTCAGGAGAGACAG 711
Db 668 TTTATTTTACATTTCTATGTGCAATGAGAAACACATAAGTTTCAGGAGCAGAGG 727
Qy 712 TACAGCTTCCAAAGCGGCTCTTGTGTATAACGGGCGTGTCTTCTTTGATGTGGCGCCT 771
Db 728 TATAGCCTTTTCAAGCTTGTCTTGGCCATAATGGTAGTCTTCTCTCTGATGTGGCGGCC 787
Qy 772 TACAACACTGTGCTTCTCTGCTGCTTCCAGGAGACACTTGTCCCTGCAGGATGAGAG 831
Db 788 TACAATATTGCAATTTTCTGTGCACTTTCAAGAACACACTTCTCCCTGAGTGACTGCAAG 847
Qy 832 AGCAGCTACCACTGGAGCGCAAGTGTTCAGGTACACAGCTGGTAGCGACCACTGTC 891
Db 848 AGCAGCTACATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACTGTC 907
Qy 892 TGGTCAACCGCTGCTCTATTGCTTCTTCAACCGGAGGCGCTTATGAGATACCTTGC 951
Db 908 TGCATCAACCTCTCTCTGATGCGTTCCTGATGGGA---CATTTAGCAATACCTCTGC 964
Qy 952 AGCTGTGTCCACCGTGCAATGATATCCCTATCAAGTAGTGGAGGCTATCAACAAGCG 1011
Db 965 CGCTGTGTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAAGC 1024
Qy 1012 CCTCAAGGGAAGTCAATGAGGAGGCGCCATTTGAACTGTACAGCAATTTGCAATCAAGGCGAG 1071
Db 1025 ACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCCAATGCA 1084
Qy 1072 GA 1073
Db 1085 GA 1086
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RESULT 12

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US-10-223-089-15
; Sequence 15, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowaki, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC9
; CURRENT APPLICATION NUMBER: US/10/223,089
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
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; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-089-15

Query Match 39.0%; Score 422; DB 15; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGATTAACATACACAGTGGCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 29 ATGSCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCC---TCATAGAAGTGCA 85
Qy 61 CTGGAACAAGTGGGCGGACCAAGTT-----CCGGCCCCGAGTTCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGACATGTGACAAGTATGACGCCAGGCACTCTCAGCCAG 145
Qy 115 CAGTGTCTGAGTCTCTCGCGGTGTTGCGGTGCTCTTGGCAACAGTGTCTGGCG 174
Db 146 CTGTGTCCATCACTCTCTCTGCTGTGTTGTATCGGTGCTCTGGACATCTCTCTGTT 205
Qy 175 GTGTTTATCTTGGTGAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAAC 234
Db 206 GTGCTTATCTCTGTTAAATATAAGGACTCAACCGCTGGAAATATCTATCTTCTTAAAC 265
Qy 235 CTGGCACTTTCAAACTGTGTTCTCTCTTCCCTCGGCTCTGGGCGCATCTAGTCAGCA 294
Db 266 TTGGCAGTTTCTAACTTGTGTTCTTCTGCTTACCTCGCCCTTCTGGGCTCATGCTG- 320
Qy 295 CACGGGGAAGCCCTGSCAACGGGACCTGTAAAGTCTTGTGCGACTCCACTCTCTCGGCG 354
Db 321 -----GGGCGATCCCATGTGTGTAATAATCTCATTTGGACTGTACTCTGTGGCG 367
Qy 355 TTATACAGCGAGGTGTTTTCCAAACATCTCTCTCTGTCGAAGGATACAGGGTGTGTTTC 414
Db 368 CTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGCAAGGTAACCTAGTGTGTTTG 427
Qy 415 CAAGGGCGAC---TGGCTCTCATCTTCCAGCAGAGTGTCTGTGTATTTGTTGCGTGCATC 471
Db 428 CACAAGGGCAACTTTTTCTCAGCCAGGAGGAGGCTGCTGTGGCATCATTTACAAGTGTG 487
Qy 472 CTGGCATGGCCCATGGCTACTGTGCTCTCTTGGCCGAGTCTGTGTTTATAGCCTCGG 531
Db 488 CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTCTGCTGAATACGTTGGTTTATAACCTCAG 547
Qy 532 ATGGAAGACAGAAACACAAAGTGTGCTTTGGCAAACTCTCACTTTCTTGGCAATCGAAGCG 591
Db 548 ATGGAAGACCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTAGTCTTCTGAGTCAAAAATGATCATCTTGGTACTTGTCTTCTCTG 651
Db 608 ACATTTCTGGAAGCAATTTCTGACTTTAAAAATGAACATTTTCGGTCTTGTCTCTCCCTA 667
Qy 652 CTGGTTTTTATAATCTGCTCAGGCACTGAGGAGAGGAGAGCTTTCAGGAGAGACAG 711
Db 668 TTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGTTCAGGAGCAGAGG 727
Qy 712 TACGACCTCCACAAGCGCGCTCTTGTGTATAACGGGCGTGTCTTCTTTTGTGTTGGCGCCT 771
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Db 728 TATAGCCTTTTCAAGCTGTGTTTTGGCCATAATGGTAGTCTTCTCTGTATGGGGCC 787
QY 772 TACAACAACCTGTCTGTTTCCCTGCTGCTTTCCAGAACACCTGTGCTCCCTGAGGATGAGAAG 831
Db 788 TACAATATGCAATTTTCTGCTCCACTTTCAGAGAACACTTCTCCCTGAGTGAAGTCAAG 847
QY 832 AGCAGCTACCACTGAGCGCAAGTGTTCAGGTTCACAGCTGAGGAGCACCACCTGTC 891
Db 848 AGCAGCTACCACTGAGCGCAAGTGTTCAGGTTCACATCACTAACTATCGCCACCACTGTC 907
QY 892 TGGCTCAACCCGCTGCTCTATTTGCTTCTTACCGGAGGCGCTTTATGAGATACCTTCGC 951
Db 908 TGAATCAACCCCTCTCTGATGCGTTTCTTATGGGA---CATTTAGCAATACCTCTGC 964
QY 952 AGCCTGTTCACCGGTGCAATGATATCCCTATCAAGTAGTGGAGGCTATCAGCAAGCG 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC 1024
QY 1012 CTTCAGGGAAGGTATGCGAGGCCCATTTGAACCTGTACAGCAATTTGCAATCAAGGCGAG 1071
Db 1025 ACATCGAGGGAAGAACCTGACCAATTCACCCGAAGTGTAAACTAGCATCCACCAATGCAA 1084
QY 1072 GA 1073
Db 1085 GA 1086

RESULT 13
US-10-223-081-15
; Sequence 15, Application US/10223081
; Publication No. US20030186866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3235P1C7
; CURRENT APPLICATION NUMBER: US/10/223,081
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR FILING DATE: 2000-07-20
; PRIOR FILING DATE: 2000-07-20
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 2000-08-24

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-081-15

Query Match 39.0%; Score 422; DB 16; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAAATACACAGTGGCGCCGAGCATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 29 ATGGCCAAATTAACACGCTGGCACCAGAGGATGAATATGATGTCC---TCATAGAGGTGAA 85
QY 61 CTGGACAACAGTGGCGCCGAGCAAGTT-----CGGCCCCCGAGTTCCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGCGCAGAGCAATGTGACAAAGTATGACGCCCAGCAGCTCTCAGCCAG 145
QY 115 CAGGTCTGAGAGTCTGCTGCGCGGTGTTTGGGTGGGTCTCTTGGACAACGTCGTGGCG 174
Db 146 CTGGTCCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTGCGACAATCTCTCGGTT 205
QY 175 GTGTTTATCTTGTGAAATACAAAGGACCTCAAGAATCTGGGGAACATCTACTTCTTAAAC 234
Db 206 GTGCTTATCTGTGTAATAATTAAGGACTCAACCGGTGGAATAATATCTATCTTCTTAAAC 265
QY 235 CTGGCACTTTTCAAACTGTGTTTCTGTCTTCCCTGCTCCCTGCTTGGGCCCATCTATGACGA 294
Db 266 TTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCGCTTCTGCGCTCATGCTG---- 320
QY 295 CACGGGGAAGCCCTGCGAAACGGGACCTGTAAAGTTCTTGTGGACTCACTCTCGGGC 354
Db 321 -----GGGGCGATCCCATGTGTAAAAATTTCTATTGGACTTACTTTCGTGGGC 367
QY 355 TTATACAGCGAGTGTGTTTCCCAACATCTCTCTGTCAGAGGATACAGGAGTGTGTTTCC 414
Db 368 CTGTACAGTGAACATTTTCAATTGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTG 427
QY 415 CAAGGCGGAC---TGCCCTCCATCTTTCAGACAGTGTCTTGTGGTATTTGTTCGTGCATC 471
Db 428 CACAAGGCAACTTTTCTCAGCCAGGAGGAGTGTGCTGCGCATCTTACAGTGTGTC 487
QY 472 CTGGCATGGGCACTGCTACTGCGCTCTCTTGGCCGAGTCTGTGTTTATGAGCTCGG 531
Db 488 CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTGCTGCAATACGTTGTTTATAAAACCTCAG 547
QY 532 ATGGAAGACAGAAACACAAAGTGTGCTTTGGCAACCTCACCTTCTTGGCAATCGAAGCG 591
Db 548 ATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAAGAACTCCCTTCTGCCAGCTGATGAG 607
QY 592 CGCTCTGGAAGTACCTTCTGAGCTCAAAATATGATCATCTTGGTACTTGTCTTCTCTG 651
Db 608 ACATCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTCTGCTTCTTGTCTCCCTA 667
QY 652 CTGGTTTTTATATCTGCTGAGGCAACTGAGAGAGGAGGAGGAGTTCAGGAGAGACAG 711
Db 668 TTTATTTTATACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGTTTCAGGAGGAGAGG 727
QY 712 TAGGACCTCCACAAAGCGGCTCTTGTCAATAACGGGGGTGTTCTCTTGTGTTGTTGGGCGCT 771
Db 728 TATAGCTTTTCAAGCTGTGTTTGGCAATATGTTAGTCTTCTCTGATGTGGGGGCC 787
QY 772 TACAACACATGTGCTTTTCTGCTGCTTTTCCAGGAACACTTGTCTCTGCAAGTATGAAG 831
Db 788 TACAATATTTGCAATTTTCTCTGCTCACTTTCAAAGAACACTTCTCTCTGAGTGAAGTCAAG 847
QY 832 AGCAGTACCACTGCAACGCAAGTGTTCAGGTTCACAGCTGTGTAGGACCACTGCTGC 891
Db 848 AGCAGTCACAATCTGGAACAAAAGTGTTCATCACTAACTATCGCCACCACTGCTGC 907
QY 892 TGGTCAACCCGCTGCTCTATTTGCTTCTTACCGGAGGCGCTTTATGAGATACCTTTCGC 951

Db 908 TGCATCAACCTCTCTCTATGCGTTTCTTGATGGGA---CATTTAGCAAAATACCTCTGC 964
Qy 952 AGCCTGTTCCACCGTGAATGATATCCCTATCAAGTAGTGGAGGTATCAGCAAGCG 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGC 1024
Qy 1012 CCTCAAGGGAAGGTCTATGCGAGGCGCCCATTTGAACTGTACAGCAATTTTGCATCAAAAGGCG 1071
Db 1025 ACATCGAGGGAAGAACCTTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAATGCAA 1084
Qy 1072 GA 1073
Db 1085 GA 1086

RESULT 14

US-10-223-082-15

; Sequence 15, Application US/10223082

; Publication No. US20030191059A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary B.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Marsters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; FILE REFERENCE: P3235P1C3

; CURRENT APPLICATION NUMBER: US/10/223,082

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/213,637

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/219,556

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 60/220,624

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/220,664

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,695

; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 09/643,657

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US00/23522

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 383

; SEQ ID NO 15

; LENGTH: 1475

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-223-082-15

Query Match

Best Local Similarity 39.0%; Score 422; DB 16; Length 1475;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGATAACTACACAGTGGCCCGGACGATGAATATGATGTCTTAATCTTAGACGACTAC 60
Db 29 ATGGCCAAATTACACGCTGGGACACGAGGATGAATATGATGTCC---TCATAGAGGTGAA 85
Qy 61 CTGGAACAACAGTGGGCGGACCAAGTT-----CGGGCCCCGAGTTCTCTCTCCCCCAG 114
Db 86 CTGGAGAGCGATGAGGCGAGCAATGTGACAAGTATGACGCCCGAGGCACTCTCAGCCAG 145
Qy 115 CAGGTGCTGCAAGTCTCTCTGCGCGTGTGCGGTCTCTTGGACAACAGTGTCTGCGG 174
Db 146 CTGTGCCATCAGTCTCTCTCTGCTGTGTTGTGATCGGTGTCTGGACAATCTCTCTGTT 205
Qy 175 GTGTTTATCTTTGGTGAATACAAAGGACTCAAGAACTCTGGGGAAACATCTACTCTCTAAAC 234
Db 206 GTGCTTATCTCTGTTAAATAATAAAGGACTCAACCGGTGGAATAATCTATCTCTCTAAAC 265
Qy 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGGTTCTGGGCCATCTATCGCAGA 294
Db 266 TTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCTCGCCCTCTCGGGCTCATGCTG----- 320
Qy 295 CACGGGAAAGCCCTGCGCAACGGGACCTGTAAAGTTCTTGTGCGACTCCACTCTCTCGGCG 354
Db 321 -----GGGGGATCCCATGTGTHAAAATTTCTCATTTGACTGTACTTCTGTGGC 367
Qy 355 TTATACAGCGAGGTGTTTCCAAACATCTCTCTCTTGTGCAAGGATACAGGGTGTGTTTCC 414
Db 368 CTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAAAGTACTACTAGTGTGTTTG 427
Qy 415 CAAGGGCGAC---TGGGCTCCATCTTCAAGCAGTGTCTTGTGGTATTTGTTGCGTGCATC 471
Db 428 CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTTACAAGTGTCT 487
Qy 472 CTGGCATGGGCAATGGCTACTCGGCTCTCTTTGCGCCAGTCTGTGTTTATATGAGCCTCGG 531
Db 488 CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTGCTGTAACGTTGTTTATAAACCCTCAG 547
Qy 532 ATGAAAGACAGAAACAAAGTGTGCGCTTTTGGCAAACTCTACTTTCTTGGCCAATCGAAGCG 591
Db 548 ATGGAAGACCAAGAAATACAAGTGTGCAATTTAGCAGAACTCTCTTCTGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTACGTTCTGACGTCAAAAATGATCATCTTGGTACTTGTCTTCTCTCTG 651
Db 608 ACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTTCGGTCTTCTGCTCTCCCTA 667
Qy 652 CTGTTTTTATATCTCTGCTGCGCAACTGAGGAGAAAGGAGAGCTTCAGGAGAGAGACAG 711
Db 668 TTTATTTTACATTTCTATGTGCAANTGAGAAAAACACTAAGTTTCAGGAGAGAGAGG 727
Qy 712 TAGCACTCCACAGCGGCTCTTGTCAATAACGGGCGTGTCTTCTTTGATGTGGCGGCT 771
Db 728 TATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGTTAGTCTTCTTCTGATGTGGCGGCC 787
Qy 772 TACAACTGTGCTTTTCTGCTGTGCTTTCAGAAACACTTGTCTCTGACAGATGAGAG 831
Db 788 TACAATATTGCAATTTTCTGCTCCACTTTCAAGAAACACTTCTCTGAGTGAAGTGAAG 847
Qy 832 AGCAGCTACCACTGGAGCAAGTGTTCAGGTCAACAGCTGTAGGAGCACCACCACTGC 891
Db 848 AGCAGCTACAACTGAGCAAAAGTGTTCATCACTAACTCATCGCACCACCACTGC 907
Qy 892 TGGGTCAACCGCTGCTCTATTTGCTTCTTGAACGAGGCGCTTTATGAGATACCTTGC 951
Db 908 TGCAATCAACCTCTCTCTGTATGGTGTCTTGTGATGGGA---CATTTAGCAAAATACCTCTGC 964
Qy 952 AGCTGTTTCCACGGTGAATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
Db 965 CGCTGTTTTCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGC 1024
Qy 1012 CCTCAAGGGAAGGTCAATGGCAGGCCCATTTGAACTGTACAGCAATTTTGCATCAAAAGGCG 1071
Db 1025 ACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAATGCAA 1084
Qy 1072 GA 1073

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Db      1085 GA 1086
||
RESULT 15
US-10-305-654-15
; Sequence 15, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-15
Query Match      39.08; Score 422; DB 17; Length 1475;
Best Local Similarity 65.58; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy      1 ATGGATAACTACACAGTGGCGCCCGGACGATGAATATGATGTCCTTAATCTTACGACGACTAC 60
Db      |||||
Qy      29 ATGCCCAATTACACGCTGGGACGACGAGGATGATATGATGTCCTCC---TCATAGAGGTGAA 85
Db      |||||
Qy      61 CTGGACAAACAGTGGCGCGGACCAAGTT-----CCGGCCCCCGAGTTCTCTCCCCCCAG 114
Db      |||||
Qy      86 CTGGAGAGCGATGAGGCGAGAGCAATGTGACAAAGTATGACGCCCGAGGCACTCTCAGGCCAG 145
Db      |||||
Qy      115 CAGGTCTGCAGTCTCTGCTGGCGGTGTTTGGCGGTGCTCTTGGACACGTCGTGGCG 174
Db      |||||
Qy      146 CTGGTGCATCACTCTGCTCTGCTGTTTGTGATGGTGTCTCTGGACAAATCTCTGGTT 205
Db      |||||
Qy      175 GTGTTTATCTTGGTGAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAAC 234
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Search completed: June 18, 2005, 15:44:37

Job time : 760.748 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 12:14:55 ; Search time 7463 Seconds
(without alignments)
11024.649 Million cell updates/sec

Title: AF014958
Perfect score: 1698
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1675.2	98.7	1755	9	BC071682 Homo sapi
4	1633.4	96.2	1770	9	BC025717 Homo sapi
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17	1033.4	60.9	1035	9	AY337001 Homo sapi
18	1031.8	60.8	1035	6	AX521743 Sequence
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	21	981.2	57.8	1050	6	AR168095 Sequence
	22	950.2	56.0	1035	9	AF124381 Macaca mu
	23	940.4	55.4	7644	6	AX345786 Sequence
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	26	683.6	40.3	1314	4	AB119273 Sus scrof
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ALIGNMENTS

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ACCESSION AF014958
VERSION AF014958.1 GI:2305263
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1698)
AUTHORS Ansari-Lari, M.A., Liu, X.-M., Gorrell, J.H. and Gibbs, R.A.
TITLE Haplotype analysis of a gene cluster containing CCR5 and a new member of chemokine receptor gene family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1698)
AUTHORS Ansari-Lari, M.A., Liu, X.-M., Gorrell, J.H. and Gibbs, R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1997) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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AUTHORS	Gish, K., McClanahan, T. K. and Moore, K. W.			Qy	601	CAGTGAGACATTTTCAATTTGCCCTCTGACTGTGCAAGGCTACTAGTGTGTCACAA	660
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AUTHORS	Gish, K., McClanahan, T. K. and Moore, K. W.			Qy	721	ATGGGTAAACAGCATTTCTGGCCACTTTTGGCTGTAATACGTGGTTTATAAACCCTCAGATGGA	780
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McDowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J. W.,
Tsurgeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 49 Row: 0 Column: 13
This clone was selected for full length sequencing because it
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gene

CDS

ORIGIN

Query Match 96.2%; Score 1633.4; DB 9; Length 1770;
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RESULT 5
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Sequence 15 from Patent WO0208284.
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AX454430
VERSION
AX454430.1 GI:21713839
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.P., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITILE
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL
Patent: WO 0208284-A 15 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

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REFERENCE 1
AUTHORS Pettipher, R.
TITLE Receptor proteins
JOURNAL Patent: WO 2004083232-A 1 30-SEP-2004;
Oxagen Limited (GB)
FEATURES
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Best Local Similarity 99.8%; Pred. No. 0;
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AX549068
LOCUS Sequence 353 from Patent WO02061087.
DEFINITION AX549068
ACCESSION AX549068
VERSION AX549068.1 GI:25813844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL	Patent: WO 02061087-A 353 08-AUG-2002;
LifeSpan Biosciences, Inc. (US)	
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LOCUS	Sequence 6461 from Patent WO0194629.
DEFINITION	AX335952
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KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE	Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL	Patent: WO 0194629-A 6461 13-DEC-2001;
FEATURES	Avalon Pharmaceuticals (US)
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VERSION U97123.1 GI:2897070
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REFERENCE
1 (bases 1 to 1645)
AUTHORS Fan, P., Kyaw, H., Su, K., Zeng, Z., Augustus, M., Carter, K. C. and Li, Y.
TITLE Cloning and characterization of a novel human chemokine receptor
JOURNAL Biochem. Biophys. Res. Commun. 243 (1), 264-268 (1998)
MEDLINE 98139902
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2 (bases 1 to 1645)
AUTHORS Fan, P., Kyaw, H., Su, K., Shell, B. K., Augustus, M., Carter, K. C. and Li, Y.
TITLE Direct Submission
JOURNAL Submitted (11-APR-1997) Protein Therapeutics, Human Genome
Sciences, Inc., 9410 Key West Ave., Rockville, MD 20850, USA
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ACCESSION QY714577
VERSION QY714577.1 GI:42275434
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
AUTHORS Kites, such as nucleic acid arrays, comprising a majority of
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Patent: WO 02068579-A 511 06-SEP-2002;
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QY 1259 AGGGAAGACCTGACCACTCCACCGAGTGTAACTAGCATCCACCAATGCAAGAGAA 1318
DB 1204 AGGGAAGACCTGACCACTCCACCGAGTGTAACTAGCATCCACCAATGCAAGAGAA 1263
QY 1319 TAAACATGGATTTTCTCTGCAATTTTCTCATGTAAATTTTCTACACATTTGTATAC 1378
DB 1264 TAAACATGGATTTTCTCTGCAATTTTCTCATGTAAATTTTCTACACATTTGTATAC 1323
QY 1379 AAAATCGGATACAGGAAGAAAGGAGAGTGTAACTAATTTGCTAAGCACTGAATTTG 1438
DB 1324 AAAATCGGATACAGGAAGAAAGGAGAGTGTAACTAATTTGCTAAGCACTGAATTTG 1383
QY 1439 TCTCAGCACCGTGAAGGCTCTTTACACGTTGAGTCTCTCGCTCTTACCACCTGTC 1498
DB 1384 TCTCAGCACCGTGAAGGCTCTTTACACGTTGAGTCTCTCGCTCTTACCACCTGTC 1443
QY 1499 CATAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAAATTAAGGCGCGGAATTTG 1558
DB 1444 CATAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAAATTAAGGCGCGGAATTTG 1503
QY 1559 TCTAAGATCACTTAACATGAGAGTGTGAGAACTGATTTCTCCAGCCCTGTGATTTGCT 1618
DB 1504 TCTAAGATCACTTAACATGAGAGTGTGAGAACTGATTTCTCCAGCCCTGTGATTTGCT 1563
QY 1619 CAGAGCTACCTTGTGTCAGACATCAAACTCCAACTCTGGGCAACAGCATGAA 1678
DB 1564 CAGAGCTACCTTGTGTCAGACATCAAACTCCAACTCTGGGCAACAGCATGAA 1623
QY 1679 TAAATGTATTTTAAACATC 1698

Db 1624 TAAATGTATTTTAAACATC 1643

RESULT 13

AC098613

LOCUS

DEFINITION

AC098613

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E.D.

Direct Submission

Unpublished

2 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (26-OCT-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E.D.

Direct Submission

Submitted (01-AUG-2002) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

On Aug 1, 2002 this sequence version replaced gi:16445164.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchg@u.washington.edu

----- Project Information

Center project name: chr-3

Center clone name: RP11-24F11 (bc0137)

----- Summary Statistics

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET; 93% of reads

Chemistry: Dye-terminator Big Dye; 7% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 184860 bases at least Q40

Consensus quality: 185398 bases at least Q30

Consensus quality: 185435 bases at least Q20

Insert size: 185437; sum-of-contigs

Quality coverage: 7.6x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': BAC-110P12 U95626, 111014-bp overlap

3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an

alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were

covered by at least one plasmid subclone or more than one M13

AC098613 185437 bp DNA linear PRI 01-AUG-2002
Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.

AC098613 2 GI:22038607

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E.D.

Direct Submission

Unpublished

2 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (26-OCT-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E.D.

Direct Submission

Submitted (01-AUG-2002) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

On Aug 1, 2002 this sequence version replaced gi:16445164.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: uwgchg@u.washington.edu

----- Project Information

Center project name: chr-3

Center clone name: RP11-24F11 (bc0137)

----- Summary Statistics

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET; 93% of reads

Chemistry: Dye-terminator Big Dye; 7% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 184860 bases at least Q40

Consensus quality: 185398 bases at least Q30

Consensus quality: 185435 bases at least Q20

Insert size: 185437; sum-of-contigs

Quality coverage: 7.6x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': BAC-110P12 U95626, 111014-bp overlap

3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:

all regions were either double-stranded or sequenced with an

alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing

problems, such as compressions and repeats; all regions were

covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII			ECORI			HindIII		
SeqDerMap	FngrPrnt		SeqDerMap	FngrPrnt		SeqDerMap	FngrPrnt	
11786	12040	8696	8937		9531	94233		
2067	2065	6	<800		6382	65011		
5681	5720	1846	1824		512	<800		
3716	3953	4052	3986		449	<800		
875	897	1159	1130		6692	65011		
910	897	54	<800		10449	10229		
2169	2215	560	<800		953	1025		
1705	1653	2287	2267		3124	3176		
5763	5720	4905	4891		1054	1025		
5844	5720	3049	3078		3985	3998		
5061	5001	1377	1394		1100	1025		
2625	2640	9903	9772		124	<800		
725	<800	1022	1021		2671	2693		
1173	1161	12606	12503		1948	1968		
5747	5720	866	868		83	<800		
9995	9684	9817	9772		7455	7474		
999	999	3598	3601		1305	1267		
4541	4503	452	<800		1047	1025		
2950	2981	7549	7635		3299	3301		
406	<800	2063	2075		5279	5237		
3375	3602	5837	5858		6815	6926		
13024	13045	13685	13328		435	<800		
416	<800	4104	3986		2509	2576		
10298	10140	1943	1928		2218	2172		
1478	1452	3964	3986		3797	3802		
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205	<800	167	<800		16192	16442		

[illegible]

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Db	65851	CATAGTGTGGATAGACTAGTCTCATTTCTCTGAGAAGAAAACCTAGCGCGGAAATTTG	65910
Qy	1559	TCTAAGATCACCTTAACCTAGGAAAGTGGCAGAACTGATTTCTCCAGCCCTGGTAGCATTTGCT	1618
Db	65911	TCTAAGATCACATACTAGGAAAGTGGCAGAACTGATTTCTCCAGCCCTGGTAGCATTTGCT	65970
Qy	1619	CAGAGCCTACGTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAACGACATGAAA	1678
Db	65971	CAGAGCCTACGTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAACGACATGAAA	66030
Qy	1679	TAAATGTATTTTAAACATC	1698
Db	66031	TAAATGTATTTTAAACATC	66050
RESULT 14			
LOCUS	AF015524	1546 bp	mRNA linear PRI 07-SEP-1998
DEFINITION	Homo sapiens putative chemokine receptor (CRAW-A) mRNA, complete cds.		
ACCESSION	AF015524		
VERSION	AF015524.1	GI:3550066	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1546)		
TITLE	Gish, K., McClanahan, T. K. and Moore, K. W.		
JOURNAL	CRAW: A Novel Human Chemokine Receptor-Like Gene Expressed in Activated Monocytes		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1546)		
TITLE	Gish, K., McClanahan, T. K. and Moore, K. W.		
JOURNAL	Direct Submission		
FEATURES	Submitted (22-JUN-1997) Molecular Biology, DNAX Research Institute, 901 California Avenue, Palo Alto, CA 94304, USA		
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	/protein_id="AAC34601.1"		
	/db_xref="GI:3550067"		
	/translation="MIYTRFLKGLSKMANYTLAPEDVDVLEGELESDEAEQCKYD AQAASQALVPSLCSKAVIFGLVDNLVLILVKYGLKRVENIYLLNLAVSNLCPLLT LPFWHAGDPMSCALFVGLVYSETFFNCLLTQVRYLFLHKGNFPSARRRVPQC IITSVLWATLAILPFWVYKQMDQKYKAFSRVTPFLPADETFWKHFLTQKNI SVLVLPFIPTFLVQMRKTRPREQRYSLKLVFVWVFLMMWAPYNIAPFLSTPK EHFSLSDCKSYNLDKSVHITKLIATHTCCINPLLYAFLDGTFYSKLCRCPHLRSNTP LQPRGQSAQGSREPDHSTVE"		
ORIGIN			
Query Match	85.3%	Score 1449.2;	DB 9; Length 1546;
Best Local Similarity	99.8%	Pred No. 0;	
Matches 1451;	Conservative	0; Mismatches	3; Indels 0; Gaps 0;
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Db	433	GAGACATTTTCAATTGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGCAAGGGC	492
QY	665	AACTTTTCTCAGCAGGAGGGTCCCTGTGGCATCAATTACAAGTGTCTGGCATGG	724
Db	493	AACTTTTCTCAGCAGGAGGGTCCCTGTGGCATCAATTACAAGTGTCTGGCATGG	552
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QY	785	CAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGG	844
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QY	845	AAGCATTTTCTGACTTTTAAATGAACATTTCCGTTCTTGTCTCTCCCTTATTTATTTT	904
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QY	905	ACATTTCTCTATGTGCAATGAGAAAACACTAAGGTTCAAGGAGCAGAGGTATAGCCTT	964
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QY	1385	GGATACAGGAAGAAAGGAGAGGTGAGCTAACATTTGTAGCACTGAATTTGTCTCAG	1444
Db	1213	GGATACAGGAAGAAAGGAGAGGTGAGCTAACATTTGTAGCACTGAATTTGTCTCAG	1272
QY	1445	GCACGCTGCAAGCTCTTTACAAAAGTGTGCTCTTCCGCTCTTACCACTTGTCCATAGT	1504
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QY	1505	GTGGATAGGACTAGTCTCATTTTCTGTAGAAAGAACTAAGCGCGGAAATTTGTCTAAG	1564
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QY	1565	ATCATTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGTAGCATTTGCTCAGAGC	1624
Db	1393	ATCATTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGTAGCATTTGCTCAGAGC	1452
QY	1625	CTACGCTTGGTCCAGAACATCAAACTCCAAACGCTGGGACAAACGACATGAATAATG	1684
Db	1453	CTACGCTTGGTCCAGAACATCAAACTCCAAACGCTGGGACAAACGACATGAATAATG	1512

QY 1685 TATTTTAAACAT 1697
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Db 1513 TATTTTAAACAT 1525
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Search completed: June 18, 2005, 18:05:07
Job time : 7470 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 12:08:05 ; Search time 957 Seconds
(without alignments)
10503.366 Million cell updates/sec

Title: AF014958
Perfect score: 1698
Sequence: 1 AGACGCTTCAGATCCTCT.....TAAATGATTTTAAACATC 1698

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*

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3: Geneseqn2000s:*

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5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

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10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1468.4	86.5	1475	6	ABL95568 Human ang
5	1468.4	86.5	1475	10	ADD10304 Human sec
6	1468.4	86.5	1475	10	ADD11264 Human sec
7	1468.4	86.5	1475	10	ADD37057 Human sec
8	1468.4	86.5	1475	12	ADB411265 Human sec
9	1468.4	86.5	1475	12	ADH43448 Human PRO
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25	1455.2	85.7	149412	3	AAA35151	Aaa35151 Human ade
26	1455.2	85.7	152739	11	ABD20816	Abd20816 Human pul
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34	1268	74.7	1270	12	ADI55954	Adi55954 Human pol
35	1267.6	74.7	1316	2	AAT99543	Aat99543 Human che
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ALIGNMENTS

RESULT 1
ADP13564
ID ADP13564 standard; DNA; 1698 BP.
XX
AC ADP13564;

DT 26-AUG-2004 (first entry)

DE Renal cell carcinoma differentially expressed gene #300.

XX ds; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression.

XX OS Homo sapiens.

XX PN WO2004048933-A2.

XX PD 10-JUN-2004.

XX PF 21-NOV-2003; 2003WO-US037481.

XX PR 21-NOV-2003; 2002US-0427982P.

PR 03-APR-2003; 2003US-0459782P.

PA (AMHP) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER J A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.
PS Disclosure; SEQ ID NO 300; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a gene that
CC is differentially expressed and detected by the method of the invention.
CC (Note: this sequence is not given as part of the printed specification
CC but was obtained from WIPO in electronic format at
CC ftp.wipo./pub/published_pct_sequences).

XX SQ Sequence 1698 BP; 434 A; 413 C; 392 G; 459 T; 0 U; 0 Other;

Query Match 100.0%; Score 1698; DB 12; Length 1698;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1698; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACGGTTCAGAGATCTCTGGAGGCTGGGGAGCTTTTGGAGTACTTTATTTCAAGTTGG 60
DB 1 AGACGGTTCAGAGATCTCTGGAGGCTGGGGAGCTTTTGGAGTACTTTATTTCAAGTTGG 60

QY 61 TCCTTGAGTCTGGTGGAGTGGGGGCTAGAGCCACAGGGGAATCAACAGTGTGTTTCG 120
DB 61 TCCTTGAGTCTGGTGGAGTGGGGGCTAGAGCCACAGGGGAATCAACAGTGTGTTTCG 120

QY 121 TGCCCCCTCAGGTCAGGAGCAGTCTGATCAAAAGAGGGCATCCACTGTCCGGGGCCATT 180
DB 121 TGCCCCCTCAGGTCAGGAGCAGTCTGATCAAAAGAGGGCATCCACTGTCCGGGGCCATT 180

QY 181 CCCACAGTCTCCGGATGCTGGGTCTGGAGGCTGGCCCTTCCCTGCGAGGAGCTCAGCCC 240
DB 181 CCCACAGTCTCCGGATGCTGGGTCTGGAGGCTGGCCCTTCCCTGCGAGGAGCTCAGCCC 240

QY 241 AGTGGCAGTCTGAAGTGGCCAAATTCACGCTGGCCACAGAGGATGAATATGATGTCCT 300
DB 241 AGTGGCAGTCTGAAGTGGCCAAATTCACGCTGGCCACAGAGGATGAATATGATGTCCT 300

QY 301 CATAGAAGTGAATCTGGAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACCCAGGC 360
DB 301 CATAGAAGTGAATCTGGAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACCCAGGC 360

QY 361 ACTCTCAGCCAGCTGGTGCCATCACTGTGCTGTGCTGTGTTGTGATCGGTGTCCTGGA 420
DB 361 ACTCTCAGCCAGCTGGTGCCATCACTGTGCTGTGCTGTGTTGTGATCGGTGTCCTGGA 420

QY 421 CAATCTCTGGTGTGCTTATCTGTGTAATAATTAAGGACTCAAAAGGCTGGAATAAT 480
DB 421 CAATCTCTGGTGTGCTTATCTGTGTAATAATTAAGGACTCAAAAGGCTGGAATAAT 480

QY 481 CTATCTTTAAACTTTGGCAGTTTCAACTGTGTTTCTTGTCTTACCTGCCCTTCTGGGC 540
DB 481 CTATCTTTAAACTTTGGCAGTTTCAACTGTGTTTCTTGTCTTACCTGCCCTTCTGGGC 540

QY 541 TCATGCTGGGGGATCCCATGTGTAAATTTCTCATTTGACATGTACTTGTGGGCTGTA 600
DB 541 TCATGCTGGGGGATCCCATGTGTAAATTTCTCATTTGACATGTACTTGTGGGCTGTA 600

QY 601 CAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTCACAA 660
DB 601 CAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTTCACAA 660

QY 661 GGGCAACTTTTCTCAGCCAGGAGGGTGGCCCTGTGGCATCATTTACAAGTGTCTGGC 720
DB 661 GGGCAACTTTTCTCAGCCAGGAGGGTGGCCCTGTGGCATCATTTACAAGTGTCTGGC 720

RESULT 2
ADQ38350
ID ADQ38350 standard; DNA; 1776 BP.

QY 721 ATGGGTAAACAGCATTCTGGCCACTTTTGCCTGATACGTTGTTTAAACCTCAGATGA 780
DB 721 ATGGGTAAACAGCATTCTGGCCACTTTTGCCTGATACGTTGTTTAAACCTCAGATGA 780

QY 781 AGACAGAAATACAAAGTGTGATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATT 840
DB 781 AGACAGAAATACAAAGTGTGATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATT 840

QY 841 CTGGAAGCATTTTCTGACTTTTAAAAATGAAATTCGGTTCCTGCTCCCTATTTAT 900
DB 841 CTGGAAGCATTTTCTGACTTTTAAAAATGAAATTCGGTTCCTGCTCCCTATTTAT 900

QY 901 TTTTACATTTCTCTATGTGCAATAGAGAAACACTAAGTTTCAGGGAGCAGAGTATAG 960
DB 901 TTTTACATTTCTCTATGTGCAATAGAGAAACACTAAGTTTCAGGGAGCAGAGTATAG 960

QY 961 CCTTTTCAAGCTTGTGTTTGGCATATGTTAGTCTTCTCTCTGATGTGGGGCCCTACAA 1020
DB 961 CCTTTTCAAGCTTGTGTTTGGCATATGTTAGTCTTCTCTCTGATGTGGGGCCCTACAA 1020

QY 1021 TATTGCAATTTTCTGTCTCACTTTTCAAGAAACACTTCTCCCTGAGTGAATGAGAG 1080
DB 1021 TATTGCAATTTTCTGTCTCACTTTTCAAGAAACACTTCTCCCTGAGTGAATGAGAG 1080

QY 1081 CTACAACTGACAAAGTGTTCATCACTAATCACTATCGCCACCCCACTGCTGCAT 1140
DB 1081 CTACAACTGACAAAGTGTTCATCACTAATCACTATCGCCACCCCACTGCTGCAT 1140

QY 1141 CAACCTCTCTGTATGTTTCTTGTAGGAGCATTTAGCAAAATACCTCTGCGCTGTTT 1200
DB 1141 CAACCTCTCTGTATGTTTCTTGTAGGAGCATTTAGCAAAATACCTCTGCGCTGTTT 1200

QY 1201 CCATCTCGTGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCACAAAGGCACATCGAG 1260
DB 1201 CCATCTCGTGTAGTAAACCCCACTTCAACCCAGGGGCGAGTCTGCACAAAGGCACATCGAG 1260

QY 1261 GGAAGAACTGACCAATTCACCGAAGTGTAACTAGCATCCCAAAATGCAAGAGAAATA 1320
DB 1261 GGAAGAACTGACCAATTCACCGAAGTGTAACTAGCATCCCAAAATGCAAGAGAAATA 1320

QY 1321 AACATGATTTTCTGCTGATTTTCTGATTAATTTCTACACATTTGTATACAA 1380
DB 1321 AACATGATTTTCTGCTGATTTTCTGATTAATTTCTACACATTTGTATACAA 1380

QY 1381 AATCGATACAGGAAGAAAGGAGAGGTAACTTTGCTTAAGCACTGAATTTGTC 1440
DB 1381 AATCGATACAGGAAGAAAGGAGAGGTAACTTTGCTTAAGCACTGAATTTGTC 1440

QY 1441 TCAGGACCGGTGCAAGGCTCTTACAAACGTGAGCTCCTCGCTCCCTACCACTTGTCCA 1500
DB 1441 TCAGGACCGGTGCAAGGCTCTTACAAACGTGAGCTCCTCGCTCCCTACCACTTGTCCA 1500

QY 1501 TAGTGTGATAGGACTAGTCTCATTTCTGAGAGAAACTTAAGCGCGGAAATTTGTC 1560
DB 1501 TAGTGTGATAGGACTAGTCTCATTTCTGAGAGAAACTTAAGCGCGGAAATTTGTC 1560

QY 1561 TAAGATCACTTAACTAGGAAGTGGAGAACTGATTTCTCAGCCCTGGTAGCATTTGCTCA 1620
DB 1561 TAAGATCACTTAACTAGGAAGTGGAGAACTGATTTCTCAGCCCTGGTAGCATTTGCTCA 1620

QY 1621 GAGCCTACGCTTGGTCCAGAACTCAAACTCCAAACCTGGGGCAAAACGACATGAATA 1680
DB 1621 GAGCCTACGCTTGGTCCAGAACTCAAACTCCAAACCTGGGGCAAAACGACATGAATA 1680

QY 1681 AATGATTTTAAACATC 1698
DB 1681 AATGATTTTAAACATC 1698

XX AC ADO38350;
 XX DT 18-NOV-2004 (first entry).
 XX DE Human SNP containing myocardial infarction-associated gene, SEQ ID 13.
 XX DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 XX KW cardiact; gene therapy; human; gene; ds.
 XX OS Homo sapiens.
 XX PN WO2004058052-A2.
 XX PD 15-JUL-2004.
 XX PF 22-DEC-2003; 2003WO-US040978.
 XX PR 20-DEC-2002; 2002US-0434778P.
 XX PR 10-MAR-2003; 2003US-0453135P.
 XX PR 30-APR-2003; 2003US-0466412P.
 XX PR 23-SEP-2003; 2003US-0504955P.
 XX PA (APPL-) APPLERA CORP.
 XX PI Cargill M, Devlin JJ, Takoubova O;
 XX WIPI; 2004-533949/51.
 XX DR P-PSDB; ADO39178.
 XX PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX Claim 7; SEQ ID NO 13; 145pp; English.
 XX The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC polynucleotide sequence represents a human myocardial infarction-
 CC associated gene containing one or more SNPs of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX SQ Sequence 1776 BP; 456 A; 425 C; 412 G; 472 T; 0 U; 11 Other;
 Query Match 99.7%; Score 1693.6; DB 13; Length 1776;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1687; Conservative 11; Mismatches 0; Indels 0; Gaps 0;
 1 AGACGCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGGTACTTTTATTTCAGTTGG 60
 72 AGACGCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGGTACTTTTATTTCAGTTGG 131

QY 61 TCCCTGAGCTCGGTGAGTGGGGCGGTAGAGCCACCCAGGGGAATCAACAGTGGTTCCTCG 120
 DB 132 TCCCTGAGCTCGGTGAGTGGGGCGGTAGAGCCACCCAGGGGAATCAACAGTGGTTCCTCG 191
 QY 121 TGGCCCTCAGGGTCAAGAGAGAGTCTGATCAAAAGAGAGGAGGATCCATCTGTCGGGGGCCATT 180
 DB 192 TGGCCCTCAGGGTCAAGAGAGAGTCTGATCAAAAGAGAGGAGGATCCATCTGTCGGGGGCCATT 251
 QY 181 CCCACAGCTCCGGATGCTGGGGTCTGGAGGCTGGGCCCTTCCCTCGCAGGAGTCCAGCCC 240
 DB 252 CCCACAGCTCCGGATGCTGGGGTCTGGAGGCTGGGCCCTTCCCTCGCAGGAGTCCAGCCC 311
 QY 241 AGTGGCAGTCTGAAGATGGCCAAATTAACAGCTGGCACCAGAGAGATGAATATATATATATAT 300
 DB 312 AGTGGCAGTCTGAAGATGGCCAAATTAACAGCTGGCACCAGAGAGATGAATATATATATATAT 371
 QY 301 CATAGAAGGTGAATCTGGAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCCAAGGC 360
 DB 372 CATAGAAGGTGAATCTGGAGAGCGATGAGGAGAGCAATGTGACAAAGTATGACGCCCAAGGC 431
 QY 361 ACTCTCAGCCAGCTGGTGGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 DB 432 ACTCTCAGCCAGCTGGTGGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
 QY 421 CAATCTCTGGTGTGCTTATCTCTGTAATAATAAAGGACTCAAAACGGCTGGAAATATAT 480
 DB 492 CAATCTCTGGTGTGCTTATCTCTGTAATAATAAAGGACTCAAAACGGCTGGAAATATAT 551
 QY 481 CTATCTTTAAACTTTGGCAGTTCTTAACTTTGTTGTTTCTGTTTACCTGCTGCTGCTGCTGCTG 540
 DB 552 CTATCTTTAAACTTTGGCAGTTCTTAACTTTGTTGTTTCTGTTTACCTGCTGCTGCTGCTGCTG 611
 QY 541 TCATGCTGGGGCGGATCCCATGTGTAAATTTCTCATTTGAGCTGTACTTCTGTTGGGCTGTA 600
 DB 612 TCATGCTGRRGGCGATCCCATGTGTAAATTTCTCATTTGAGCTGTACTTCTGTTGGGCTGTA 671
 QY 601 CAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTGGACAA 660
 DB 672 CAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTGGACAA 731
 QY 661 GGGCAACTTTTCTCAGCAGAGAGAGGGTGGCTGTGGCATCATTTACAAAGTGTCTCTGGC 720
 DB 732 GGGCAACTTTTCTCAGCAGAGAGAGGGTGGCTGTGGCATCATTTACAAAGTGTCTCTGGC 791
 QY 721 ATGGGTTACAGCATTCTGGCCACTTTGCTCAATACGTGGTGTATATAAACCCTCAGATGGA 780
 DB 792 ATGGGTTACAGCATTCTGGCCACTTTGCTCAATACGTGGTGTATATAAACCCTCAGATGGA 851
 QY 781 AGACCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCTGCCAGCTGATGAGACATT 840
 DB 852 AGACCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTCTGCCAGCTGATGAGACATT 911
 QY 841 CTGGAAGCATTTTCTGACTTTTAAATAAGCAATTTGGTTCCTGCTCCCTCTATTTAT 900
 DB 912 CTGGAAGCATTTTCTGACTTTTAAATAAGCAATTTGGTTCCTGCTCCCTCTATTTAT 971
 QY 901 TTTTACATTTCTCTATGTGCAATTCAGAAACACATTAAGGTTTTCAGGAGCAGAGGTATAG 960
 DB 972 TTTTACATTTCTCTATGTGCAATTCAGAAACACATTAAGGTTTTCAGGAGCAGAGGTATAG 1031
 QY 961 CCTTTTCAAGCTTGTGTTTGGCATAATGCTAGTCTTCTCTCTGATGTGGCGCCCTTACAA 1020
 DB 1032 CCTTTTCAAGCTTGTGTTTGGCATAATGCTAGTCTTCTCTCTGATGTGGCGCCCTTACAA 1091
 QY 1021 TATTCATTTTCTGCTCATTTCCTTCAAGAAACATTTCTCTCTGATGTGGAGTCTGCAAGAGCAG 1080
 DB 1092 TATTCATTTTCTGCTCATTTCCTTCAAGAAACATTTCTCTCTGATGTGGAGTCTGCAAGAGCAG 1151
 QY 1081 CTACATCTGGCAAAAGTGTTCATCACTAACTCACTGCGCCACCCACCTCCTGCTGCAT 1140
 DB 1152 CTACATCTGGCAAAAGTGTTCATCACTAACTCACTGCGCCACCCACCTCCTGCTGCAT 1211

Db 61 ATATGATGTCTCTANTAGAAAGGTGAATCTGGAGAGCGATGAGCGAGCAATGTGACAAGTA 120
Qy 349 TGACGCCACGACACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGAT 408
Db 121 TGACGCCACGACACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTGTGAT 180
Qy 409 CGGTGCTCTGGACAATCTCTCTGTTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 468
Db 181 CGGTGCTCTGGACAATCTCTCTGTTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 240
Qy 469 CGTGGAAAATATCTATCTCTTAACCTGGCAGTTTCTAACTTGTTCTGTTCTTACCCT 528
Db 241 CGTGGAAAATATCTATCTCTTAACCTGGCAGTTTCTAACTTGTTCTGTTCTTACCCT 300
Qy 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 360
Qy 589 CGTGGGCTGTACAGTGAGACATTTTCAATTCGCTTCTGACTGTGCGAAAGGTACCTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTCGCTTCTGACTGTGCGAAAGGTACCTAGT 420
Qy 649 GTTTTTGCAAGGCAACTTTTCTCAGCCAGGAGGGTGGCTGTGGCATCTTAC 708
Db 421 GTTTTTGCAAGGCAACTTTTCTCAGCCAGGAGGGTGGCTGTGGCATCTTAC 480
Qy 709 AAGTGTCTGGCATGGTAAACAGCCATTTCTGGCCACTTTGGCCCTGAATACGTGGTTTATAA 768
Db 481 AAGTGTCTGGCATGGTAAACAGCCATTTCTGGCCACTTTGGCCCTGAATACGTGGTTTATAA 540
Qy 769 ACCTCAGATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGC 828
Db 541 ACCTCAGATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGC 600
Qy 829 TGAATGACATTTCTGAGCAATTTCTGACTTTTAAATTAAGCAATTTGGTCTTGTCT 888
Db 601 TGAATGACATTTCTGAGCAATTTCTGACTTTTAAATTAAGCAATTTGGTCTTGTCT 660
Qy 889 CCCCTTATTTTATCTCTCTATGTGCAATGAGAAACACTAAGGTTCAAGGA 948
Db 661 CCCCTTATTTTATCTCTCTATGTGCAATGAGAAACACTAAGGTTCAAGGA 720
Qy 949 GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTGGCAATAATGGTAGTCTCTCTCTGATGTG 1008
Db 721 GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTGGCAATAATGGTAGTCTCTCTCTGATGTG 780
Qy 1009 GGGCCCTCAATATTTGCAATTTTCTGTGCTTCTTCAAGAACACTTCTCCTGAGTGA 1068
Db 781 GGGCCCTCAATATTTGCAATTTTCTGTGCTTCTTCAAGAACACTTCTCCTGAGTGA 840
Qy 1069 CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAACTCATGCCACCAC 1128
Db 841 CTGCAAGAGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAACTCATGCCACCAC 900
Qy 1129 CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAAAATACCT 1188
Db 901 CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAAAATACCT 960
Qy 1189 GTGCGCTGTTTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1248
Db 961 GTGCGCTGTTTCCATCTCGGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1020
Qy 1249 AGGCACATCGAGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT 1308
Db 1021 AGGCACATCGAGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT 1080
Qy 1309 GCAAGAAGATAAATCGGATTTTCACTTTCTGCAATTTTCAATGATAATTTTCTACAC 1368
Db 1081 GCAAGAAGATAAATCGGATTTTCACTTTCTGCAATTTTCAATGATAATTTTCTACAC 1140
Qy 1369 ATTTGTATCAAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAACTTTGCTAAGC 1428
Db 1141 ATTTGTATCAAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAACTTTGCTAAGC 1200

Qy 1429 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCCGCTCCT 1488
Db 1201 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCCGCTCCT 1260
Qy 1489 ACCACTTTGCTCAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAAACCTAAGGCG 1548
Db 1261 ACCACTTTGCTCAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAAACCTAAGGCG 1320
Qy 1549 CGGAATTTGTCTTAGATCACTTAACTAGGAAGTGCAGAACTGATTTCTCCAGCCCTGGT 1608
Db 1321 CGGAATTTGTCTTAGATCACTTAACTAGGAAGTGCAGAACTGATTTCTCCAGCCCTGGT 1380
Qy 1609 AGCAATTTGCTCAGAGCCTACGCTTGGTCCAGAACTCAAACTCCAAACCTGGGGACAAA 1668
Db 1381 AGCAATTTGCTCAGAGCCTACGCTTGGTCCAGAACTCAAACTCCAAACCTGGGGACAAA 1440
Qy 1669 CGACATGAAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAAATAAATGATTTTAAACATC 1470

RESULT 4

ABL95568

ID ABL95568 standard; cDNA; 1475 BP.

XX ABL95568;
AC ABL95568;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO1873 SEQ ID NO: 15.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.
PN WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00665350.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

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PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001WO-US0170574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR P-PSDB; ABB95430.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 15; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 86.5%; Score 1468.4; DB 6; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACAGCTGGCAGCAGAGATGA 288
DB 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACAGCTGGCAGCAGAGATGA 50
QY 289 ATATGATGTCCTCATAGAAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAAGTA 348
DB 61 ATATGATGTCCTCATAGAAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGGCCATCCTCTCTGCTGCTGCTTTGTGAT 408
DB 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGGCCATCCTCTCTGCTGCTGCTTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCTCTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 468
DB 181 CGGTGTCCTGGCAATCTCTCTGCTTATCTCTGGTAAATATAAAGGACTCAAAAG 240
QY 469 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTGTTGTTTCTGCTTACCCT 528
DB 241 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTGTTGTTTCTGCTTACCCT 300
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QY 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATTCTCATTTGGAGCTGACTT 588
DB |||||
DB 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATTCTCATTTGGAGCTGACTT 360
QY 589 CGTGGCCCTGTACAGTGTAGACATTTTTCATTTGCCCTTCTGACTGTGCAAAAGGTACTAGT 648
DB |||||
DB 361 CGTGGCCCTGTACAGTGTAGACATTTTTCATTTGCCCTTCTGACTGTGCAAAAGGTACTAGT 420
QY 649 GTTTTTCACAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCCCTTGGCATCATTTAC 708
DB |||||
DB 421 GTTTTTCACAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCCCTTGGCATCATTTAC 480
QY 709 AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATACGTGTTTATAA 768
DB |||||
DB 481 AAGTGTCTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATACGTGTTTATAA 540
QY 769 ACCTCAGATGGAAGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTCCAGC 828
DB |||||
DB 541 ACCTCAGATGGAAGACCAAGAAATACAAGTGTGCATTTTAGCAGAACTCCCTTCTCCAGC 600
QY 829 TGATGAGACATTTCTGGAAGCATTTTCTGCACTTTAAATGAACATTTTGGTCTTGTCT 888
DB |||||
DB 601 TGATGAGACATTTCTGGAAGCATTTTCTGCACTTTAAATGAACATTTTGGTCTTGTCT 660
QY 889 CCCCTATTTTATTTTACATTTCTATGTGCAATGAGAAACACACTAAGGTTTCAGGA 948
DB |||||
DB 661 CCCCTATTTTATTTTACATTTCTATGTGCAATGAGAAACACACTAAGGTTTCAGGA 720
QY 949 CGAGAGGTATAGCCCTTTTCAAGCTTTTGGCCATTAATGGTGTGTTTCTTCTCTGATGTG 1008
DB |||||
DB 721 CGAGAGGTATAGCCCTTTTCAAGCTTTTGGCCATTAATGGTGTGTTTCTTCTCTGATGTG 780
QY 1009 GCGCCCTACATATTGCACTTTTCTGCTCCTTTCACATTTTCAAGAAACACTTCTCCCTGAGTGA 1068
DB |||||
DB 781 GCGCCCTACATATTGCACTTTTCTGCTCCTTTCACATTTTCAAGAAACACTTCTCCCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAACTCTGGACAAAGTGTTCACATCACTAACTCATGCCACCAC 1128
DB |||||
DB 841 CTGCAAGAGCAGCTACAACTCTGGACAAAGTGTTCACATCACTAACTCATGCCACCAC 900
QY 1129 CCATGCTGCAATCAACCCCTCTCTGTATGTCGTTTCTTGTATGGGACATTTAGCAAAATACCT 1188
DB |||||
DB 901 CCATGCTGCAATCAACCCCTCTCTGTATGTCGTTTCTTGTATGGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGCTGTTTCCATCTGCTGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1248
DB |||||
DB 961 CTGCGCTGTTTCCATCTGCTGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCA 1020
QY 1249 AGGCACATCGAGGGAAGAACTCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1308
DB |||||
DB 1021 AGGCACATCGAGGGAAGAACTCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1080
QY 1309 GCAAGAAGATAAATCAATGGAATTTTTCATCTTCTGCAATTTTTCATGTAAAATTTTCTACAC 1368
DB |||||
DB 1081 GCAAGAAGATAAATCAATGGAATTTTTCATCTTCTGCAATTTTTCATGTAAAATTTTCTACAC 1140
QY 1369 ATTTGTATACAAATTCGATACAGAAAGAGGAGAGGTGAGCTACATTTGCTTAGC 1428
DB |||||
DB 1141 ATTTGTATACAAATTCGATACAGAAAGAGGAGAGGTGAGCTACATTTGCTTAGC 1200
QY 1429 ACTGAATTTGTCTCAGGCAACCGTCAAGGCTCTTTTACAAACGTGAGCTCTTTCGCTCTCT 1488
DB |||||
DB 1201 ACTGAATTTGTCTCAGGCAACCGTCAAGGCTCTTTTACAAACGTGAGCTCTTTCGCTCTCT 1260
QY 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTGTCTCAATTTTCTGTAGAAGAAACTAAGGG 1548
DB |||||
DB 1261 ACCACTTGTCCATAGTGTGGATAGGACTAGTGTCTCAATTTTCTGTAGAAGAAACTAAGGG 1320
QY 1549 CGGAATTTGTCTAAGATCACTTAATAGGAGTGGCAGAGCTGATTTCTCCAGCCCTGCT 1608
DB |||||
DB 1321 CGGAATTTGTCTAAGATCACTTAATAGGAGTGGCAGAGCTGATTTCTCCAGCCCTGCT 1380
QY 1609 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAAACATCAAACTCCAAACCCCTGGGACAAA 1668
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Db 1381 AGCAATTGGCTCAGAGCCTAGCTTGGTCCAGAACATCAAAACCTCGGGACAAA 1440
QY 1669 CGACATGAATAAATGATTTTAAAAACATC 1698
Db 1441 CGACATGAATAAATGATTTTAAAAACATC 1470

RESULT 5

ID ADD10304 standard; cDNA; 1475 BP.

XX AC ADD10304;

XX DT 01-JAN-2004 (first entry)

XX DE Human secreted/transmembrane PRO polypeptide cDNA #8.

XX KW ss; gene; human; secreted protein; transmembrane protein;
cardiovascular disorder; endothelial disorder; angiogenic disorder;
myocardial infarction; cardiac hypertrophy; trauma; cancer;
XX KW age-related macular degeneration; angiogenesis;
XX KW endothelial cell apoptosis; smooth muscle cell growth;
XX KW endothelial cell tube formation.

XX OS Homo sapiens.

XX PN US2003105011-A1.

XX PD 05-JUN-2003.

XX PF 16-AUG-2002; 2002US-00223084.

XX PR 15-SEP-2000; 2000US-0232887P.

XX PR 20-JUN-2001; 2001WO-US019692.

XX PR 09-JUL-2001; 2001WO-US021735.

XX PR 20-FEB-2002; 2002US-00081056.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX P-PSDB; ADD10305.

XX WPI: 2003-810831/76.

XX PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.

XX PS Claim 2; SEQ ID NO 15; 493pp; English.

XX CC The invention relates to an isolated nucleic acid encoding a secreted and
transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
by the nucleic acid, or an agonist or antagonist, is used to treat a
cardiovascular, endothelial, or angiogenic disorder in a mammal,
preferably a human. The human may have suffered a myocardial infarction
or has cardiac hypertrophy, trauma, a cancer, or age-related macular
degeneration. The cardiac hypertrophy is characterised by the presence of
an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
specification, or an agonist is used to inhibit or stimulate endothelial
cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO302 or an agonist is used to induce endothelial cell apoptosis. A PRO
polypeptide, given in the specification, or an agonist is used to
stimulate or inhibit smooth muscle cell growth, or to induce endothelial
cell tube formation. The present sequence represents a cDNA encoding a
PRO polypeptide of the invention.

XX SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 86.5%; Score 1468.4; DB 10; Length 1475;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 229 GGAGCTCAGCCAGGCGGCGAGTCTCAAGATGCGCCAAATACAGCTGGCACGAGAGATGA 288
Db 1 GGAGCTCAGCCAGGCGGCGAGTCTCAAGATGCGCCAAATACAGCTGGCACGAGAGATGA 60
QY 289 ATATGATGTCTCATAGAAAGGTGAATCTGGAGAGCGATGAGGAGAGCAATGTGCAAGTA 348
Db 61 ATATGATGTCTCATAGAAAGGTGAATCTGGAGAGCGATGAGGAGAGCAATGTGCAAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTGTGTGTGT 408
Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTGTGTGTGT 180
QY 409 CGGTGCTCTGGACAAATCTCTGTTGTCTTATCTCTGTTTAAATATAAAGGACTCAAAAG 468
Db 181 CGGTGCTCTGGACAAATCTCTGTTGTCTTATCTCTGTTTAAATATAAAGGACTCAAAAG 240
QY 469 CQTGAAAATATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTCTTCTTGTACCT 528
Db 241 CQTGAAAATATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTCTTCTTGTACCT 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATTTCTCATTTGAGCTGTACT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATTTCTCATTTGAGCTGTACT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCCCTCTGACTGTGCAAGAGTACTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCCCTCTGACTGTGCAAGAGTACTAGT 420
QY 649 GTTTTTCACAAAGGGCAACTTTTCTCAGCCAGGAGGAGGGTGCCTCTGTGGCATCATTTAC 708
Db 421 GTTTTTCACAAAGGGCAACTTTTCTCAGCCAGGAGGAGGGTGCCTCTGTGGCATCATTTAC 480
QY 709 AAGTGTCTGCGATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATAGCTGGTTTATAA 768
Db 481 AAGTGTCTGCGATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGAATAGCTGGTTTATAA 540
QY 769 ACCTCAGATGGAAGACACCAAGTAATCAAGTGTGCAATTTAGCAAGCTCCCTCTCGCCAGC 828
Db 541 ACCTCAGATGGAAGACACCAAGTAATCAAGTGTGCAATTTAGCAAGCTCCCTCTCGCCAGC 600
QY 829 TGATGAGACATTTCTGGAAGCAATTTTCTGCACTTTTAAATTTGAACTTTTGGTTCTGTCT 888
Db 601 TGATGAGACATTTCTGGAAGCAATTTTCTGCACTTTTAAATTTGAACTTTTGGTTCTGTCT 660
QY 889 CCCCCTATTTATTTTACATTTCTATGTGCAATGAGAAACACATCAAGGTTTCAGGA 948
Db 661 CCCCCTATTTATTTTACATTTCTATGTGCAATGAGAAACACATCAAGGTTTCAGGA 720
QY 949 GCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCCATATGTTAGTCTTCTCTGATGTG 1008
Db 721 GCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCCATATGTTAGTCTTCTCTGATGTG 780
QY 1009 GCGGCCCTTACAAATTTGCAATTTTCTGTCACACTTTTCAAGAAACACTTCTCCCTGAGTGA 1068
Db 781 GCGGCCCTTACAAATTTGCAATTTTCTGTCACACTTTTCAAGAAACACTTCTCCCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAAATCTGGAACAAAGTGTTCACATCACTAACTCATGCGCCACCAC 1128
Db 841 CTGCAAGAGCAGCTACAAATCTGGAACAAAGTGTTCACATCACTAACTCATGCGCCACCAC 900
QY 1129 CCACGTGTCATCAACCTCTCTGTTATGCGTTTCTGATGGGACATTTAGCAAAATACCT 1188
Db 901 CCACGTGTCATCAACCTCTCTGTTATGCGTTTCTGATGGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGGAGTCTGCACA 1248
Db 961 CTGCGGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGGAGTCTGCACA 1020
QY 1249 AGGCACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCACCAAT 1308

Db 1021 AGGCACATCGAGGGAAGACCTGACCATTCACCGAAGTGTAACCTAGCATCCACCAAT 1080
Qy 1309 GCAAGAGATAAATGATTTTCATCTTCTGCAATTAATTCATGTAATTTTCTACAC 1368
Db 1081 GCAAGAGATAAATGATTTTCATCTTCTGCAATTAATTCATGTAATTTTCTACAC 1140
Qy 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGCTGAGCTAACATTTGCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGCTGAGCTAACATTTGCTAAGC 1200
Qy 1429 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCTTCGCGCTCT 1488
Db 1201 ACTGAATTTGTCTCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCTTCGCGCTCT 1260
Qy 1489 ACCACTTGTCCATAGTGTGGATAGACTAGTCTCATTTCTCGAAGAAACCTAAGCG 1548
Db 1261 ACCACTTGTCCATAGTGTGGATAGACTAGTCTCATTTCTCGAAGAAACCTAAGCG 1320
Qy 1549 CGGAATTTGTCTAAGATCACCTTAAGTGAAGAGTGCAGAACTGATTTCCAGGCCCTGT 1608
Db 1321 CGGAATTTGTCTAAGATCACCTTAAGTGAAGAGTGCAGAACTGATTTCCAGGCCCTGT 1380
Qy 1609 AGCATTTGTCTCAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGACAAA 1668
Db 1381 AGCATTTGTCTCAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGACAAA 1440
Qy 1669 CGACATGAATAAATGTATTTAAACATC 1698
Db 1441 CGACATGAATAAATGTATTTAAACATC 1470

RESULT 6

ADD11264
ID ADD11264 standard; cDNA; 1475 BP.
XX AC ADD11264;
XX AC
DT 01-JAN-2004 (first entry)
XX DE Human secreted/transmembrane PRO polypeptide cDNA #8.
XX ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX OS Homo sapiens.
XX PN US2003105013-A1.
XX PD 05-JUN-2003.
XX PF 16-AUG-2002; 2002US-00223090.
XX PR 20-JUN-2001; 2001WO-US019692.
XX PR 09-JUL-2001; 2001WO-US021735.
XX PR 20-FEB-2002; 2002US-00081056.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX P-PSDB; ADD11265.
XX WPI; 2003-801242/75.
XX DR P-PSDB; ADD11265.
XX PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, useful for treating a cardiovascular, endothelial, or
PT angiogenic disorder in a mammal, such as cancer or age-related macular
PT degeneration.

XX Claim 2; SEQ ID NO 15; 493pp; English.
XX PS The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of pG-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents a cDNA encoding a
CC PRO polypeptide of the invention.
XX SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 86.5%; Score 1468.4; DB 10; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACAGCTGGCCACGAGGATGA 288
Db 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACAGCTGGCCACGAGGATGA 60
Qy 289 ATATGATGTCCTCATAGAAAGGTGAACCTGGAGCGGATGAGCAGAGCAATGTGACAAGTA 348
Db 61 ATATGATGTCCTCATAGAAAGGTGAACCTGGAGCGGATGAGCAGAGCAATGTGACAAGTA 120
Qy 349 TGAGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCCACTCTGCTCTGCTGTGTTGTGAT 408
Db 121 TGAGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCCACTCTGCTCTGCTGTGTTGTGAT 180
Qy 409 CGGTGTCTCGACAATCTCCTGGTGTGCTTATCCTGCTGTAATAATAAGGACTCAACG 468
Db 181 CGGTGTCTCGACAATCTCCTGGTGTGCTTATCCTGCTGTAATAATAAGGACTCAACG 240
Qy 469 CGTGAATAATATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCT 528
Db 241 CGTGAATAATATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCT 300
Qy 529 GCCCTTCTGGCTCATGCTGGGGCGATCCCATGFTAAATTTCTCATTTGAGCTGACTT 588
Db 301 GCCCTTCTGGCTCATGCTGGGGCGATCCCATGFTAAATTTCTCATTTGAGCTGACTT 360
Qy 589 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCTTCTGACTGTGCAAGGTACTAGT 420
Qy 649 GTTTTTCACAAGGCAACTTTTCTCAGCCAGAGGAGGGTGCCTCTGGGCATCATTTAC 708
Db 421 GTTTTTCACAAGGCAACTTTTCTCAGCCAGAGGAGGGTGCCTCTGGGCATCATTTAC 480
Qy 709 AAGTGTCTGGCTGAGGTAACAGCCATTTCTGGCCATTTTGGCTGAATACGTGTTTATAA 768
Db 481 AAGTGTCTGGCTGAGGTAACAGCCATTTCTGGCCATTTTGGCTGAATACGTGTTTATAA 540
Qy 769 ACCTCAGATGGAAGCAGCAATACAGTGTGCAATTTAGCAGCACTCCCTTCTCCGACG 828
Db 541 ACCTCAGATGGAAGCAGCAATACAGTGTGCAATTTAGCAGCACTCCCTTCTCCGACG 600
Qy 829 TGATGAGACATTTCTGGAAGCAATTTTCTGACTTTTAAAAATGAACATTTTGGTTCTTCT 888
Db 601 TGATGAGACATTTCTGGAAGCAATTTTCTGACTTTTAAAAATGAACATTTTGGTTCTTCT 660
Qy 889 CCCCTATTTATTTTACATTTCTCTATGTGCAATATGAGAAAAACACATAAGGTTCAAGGA 948
Db 661 CCCCTATTTATTTTACATTTCTCTATGTGCAATATGAGAAAAACACATAAGGTTCAAGGA 720


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Qy 949 GCAGAGTATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTCTGATGTG 1008
Db |||||
Qy 721 GCAGAGTATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTCTGATGTG 780
Db |||||
Qy 1009 GGGCCCTCAATAATGCAATTTTCCCTGTCACATTTCAAGAACACTTCTCCCTGAGTGA 1068
Db |||||
Qy 781 GGGCCCTCAATAATGCAATTTTCCCTGTCACATTTCAAGAACACTTCTCCCTGAGTGA 840
Db |||||
Qy 1069 CTGCAAGAGCAGCTACAACTCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCAC 1128
Db |||||
Qy 841 CTGCAAGAGCAGCTACAACTCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCAC 900
Db |||||
Qy 1129 CCACTGCTGCATCAACCTCTCTCTGATGCGTTCCTTGTAGTGGGACATTTAGCAAAATACCT 1188
Db |||||
Qy 901 CCACTGCTGCATCAACCTCTCTCTGATGCGTTCCTTGTAGTGGGACATTTAGCAAAATACCT 960
Db |||||
Qy 1189 CTGCGCTGTTCCATCTGCTAGTACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1248
Db |||||
Qy 961 CTGCGCTGTTCCATCTGCTAGTACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1020
Db |||||
Qy 1249 AGGCACATCAGGGAAGAACTCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAAT 1308
Db |||||
Qy 1021 AGGCACATCAGGGAAGAACTCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAAT 1080
Db |||||
Qy 1309 GCAAGAGAATAAACATGGAATTTTCATCTTCTGCAATTTTCATGTAAATTTTCTACAC 1368
Db |||||
Qy 1081 GCAAGAGAATAAACATGGAATTTTCATCTTCTGCAATTTTCATGTAAATTTTCTACAC 1140
Db |||||
Qy 1369 ATTGTATACAAATCGGATACAGGAGAGAAAAGGAGAGTGTAGCTAACTTTGCTAAGC 1428
Db |||||
Qy 1141 ATTGTATACAAATCGGATACAGGAGAGAAAAGGAGAGTGTAGCTAACTTTGCTAAGC 1200
Db |||||
Qy 1429 ACTGAATTTCTCTCAGCACCGTGCAAGGCTCTTTACAACTGAGCTCTCGCCCTCT 1488
Db |||||
Qy 1201 ACTGAATTTCTCTCAGCACCGTGCAAGGCTCTTTACAACTGAGCTCTCGCCCTCT 1260
Db |||||
Qy 1489 ACCACTTGTCTAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAAAATAAGGCG 1548
Db |||||
Qy 1261 ACCACTTGTCTAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAAAATAAGGCG 1320
Db |||||
Qy 1549 CGGAATTTGTCTAAGATCACTTAACCTAGGAAGTGGCAGAACTGTCTCCAGCCCTGGT 1608
Db |||||
Qy 1321 CGGAATTTGTCTAAGATCACTTAACCTAGGAAGTGGCAGAACTGTCTCCAGCCCTGGT 1380
Db |||||
Qy 1609 AGCATTTGCTCAGAGCTACGCTTGTGTCAGAGACATCAAACTCCAAACCTGGGGACAA 1668
Db |||||
Qy 1381 AGCATTTGCTCAGAGCTACGCTTGTGTCAGAGACATCAAACTCCAAACCTGGGGACAA 1440
Db |||||
Qy 1669 CGACATGAATAAATGTATTTTAAACATC 1698
Db |||||
Qy 1441 CGACATGAATAAATGTATTTTAAACATC 1470
Db |||||

RESULT 7
ADD37057
ID ADD37057 standard; cdna; 1475 BP.
XX
AC ADD37057;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide cdna #8.
XX
SS ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
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PN
XX
PD
XX
PF
XX
PR 15-SEP-2000; 2000US-0223088.
PR 20-JUN-2001; 2001US-0232887P.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
DR WPI; 2003-829354/77.
DR P-PSDB; ADD37058.
XX
PT New isolated nucleic acids encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS Claim 2; SEQ ID NO 15; 492pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterized by the presence of
CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents a cdna encoding a
CC PRO polypeptide of the invention.
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 86.5%; Score 1468.4; DB 10; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 229 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCAATTACACGCTGGCAGAGGATGA 288
Db 1 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCAATTACACGCTGGCAGAGGATGA 60

Qy 289 ATATGATGTCTCATAGAAAGTGAATCGAGAGCGATAGGAGAGCAATGTGCAAGTA 348
Db 61 ATATGATGTCTCATAGAAAGTGAATCGAGAGCGATAGGAGAGCAATGTGCAAGTA 120

Qy 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCAGTCTGCTGCTGTTGTGAT 408
Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCAGTCTGCTGCTGTTGTGAT 180

Qy 409 CGGTGTCTGGCAATCTCTGTTGTGCTTATCTGGTAAATAATAAAGGACTCAAAACG 468
Db 181 CGGTGTCTGGCAATCTCTGTTGTGCTTATCTGGTAAATAATAAAGGACTCAAAACG 240

Qy 469 CTTGAAATAATCTATCTTAACTTGGCAGTTTCTAACTGTGTGTTTCTTGTACCT 528
Db 241 CTTGAAATAATCTATCTTAACTTGGCAGTTTCTAACTGTGTGTTTCTTGTACCT 300

Qy 529 GGCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATCTCATTTGGACTGTACTT 588
Db 301 GGCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATCTCATTTGGACTGTACTT 360
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QY 589 CGTGGCCCTGTACGTGACACATTTTCAATTGGCTTCTGACTGTGCAAAAGGTACCTAGT 648
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 CGTGGCCCTGTACGTGACACATTTTCAATTGGCTTCTGACTGTGCAAAAGGTACCTAGT 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 649 GTTTTGTGCAAAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCAATTAC 708
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 421 GTTTTGTGCAAAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCAATTAC 480
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 709 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTTGCCTGAATAGTGGTTTATAA 768
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 481 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTTGCCTGAATAGTGGTTTATAA 540
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 769 ACCTCAGATGGAAGCAGCAAAATACAAGTGTCAATTTAGCAAACTCCCTTCCCTCCAGC 828
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 541 ACCTCAGATGGAAGCAGCAAAATACAAGTGTCAATTTAGCAAACTCCCTTCCCTCCAGC 600
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 829 TGATGAGACATTTCTGGAAGCAATTTTCTGACTTTTAAATAATGAACATTTTCGTTCTGTCT 888
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 TGATGAGACATTTCTGGAAGCAATTTTCTGACTTTTAAATAATGAACATTTTCGTTCTGTCT 660
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 889 CCCCCTATTTTATTTTACATTTCTCTATGTGCAAAATGAGAAACACATTAAGTTTCAAGGA 948
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 661 CCCCCTATTTTATTTTACATTTCTCTATGTGCAAAATGAGAAACACATTAAGTTTCAAGGA 720
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 949 GCAGAGGTATAGCTTTTCAAGCTTGTGTTTTCGCATTAATGGTAGTCTTCTCTGATGTG 1008
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 721 GCAGAGGTATAGCTTTTCAAGCTTGTGTTTTCGCATTAATGGTAGTCTTCTCTGATGTG 780
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1009 GCGCCCTCAATATTTGCAATTTTCTCTGTCACATTTTCAAGGAACACTTCTCCCTCGAGTGA 1068
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 781 GCGCCCTCAATATTTGCAATTTTCTCTGTCACATTTTCAAGGAACACTTCTCCCTCGAGTGA 840
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1069 CTGCAAGACAGCTCAATCTCGGACAAAGAGTGTTCATCACTAACTCATGCCACCAC 1128
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 CTGCAAGACAGCTCAATCTCGGACAAAGAGTGTTCATCACTAACTCATGCCACCAC 900
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1129 CCACCTGCTCATCAACCTCTCTGTCATGCTGTTTCTTGATGGACATTTAGCAAAATACCT 1188
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 901 CCACCTGCTCATCAACCTCTCTGTCATGCTGTTTCTTGATGGACATTTAGCAAAATACCT 960
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1189 CTGCGCTCTTTTCCATCTCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1248
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 961 CTGCGCTCTTTTCCATCTCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1020
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1249 AGGCATCTCGAGGAAGAACCTTGACCAATTCACCGAAGTGTAACTAGCATCCACAAT 1308
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1021 AGGCATCTCGAGGAAGAACCTTGACCAATTCACCGAAGTGTAACTAGCATCCACAAT 1080
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1309 GCAAGAAGATAAACAATGATTTTCATCTTCTGCAATTAATTCATGTAATTTTCTACAC 1368
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1081 GCAAGAAGATAAACAATGATTTTCATCTTCTGCAATTAATTCATGTAATTTTCTACAC 1140
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAACTTTGCTAAGC 1428
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAACTTTGCTAAGC 1200
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1429 ACTGAATTTGTCTCAGGCAACGCTGCAAGGCTTTTACAAACGTGAGCTCTTTCGCTCTCT 1488
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1201 ACTGAATTTGTCTCAGGCAACGCTGCAAGGCTTTTACAAACGTGAGCTCTTTCGCTCTCT 1260
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1489 ACCACTTGTCCATGTTGATAGGACTAGTCTCATTTCTCTGAGAGAAACTAAGGCG 1548
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1261 ACCACTTGTCCATGTTGATAGGACTAGTCTCATTTCTCTGAGAGAAACTAAGGCG 1320
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1549 CGGAATTTGTCTAAGATCACTTAATAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGTG 1608
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1321 CGGAATTTGTCTAAGATCACTTAATAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGTG 1380
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1609 AGCATTTGTCTAGAGCCTACGTTGTGTCAGAAACATCAAACTCCAAACCTCTGGGACAAA 1668
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1381 AGCATTTGTCTAGAGCCTACGTTGTGTCAGAAACATCAAACTCCAAACCTCTGGGACAAA 1440
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1669 CGACATGAATAAATGATTTTAAACATC 1698

Db 1441 CGACATGAATAAATGATTTTAAACATC 1470

RESULT 8

ADE41265

ID ADE41265 standard; cDNA; 1475 BP.

XX ADE41265;

XX 29-JAN-2004 (first entry)

XX Human secreted/transmembrane PRO polypeptide cDNA #8.

DE ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.

XX Homo sapiens.

XX US2003100497-A1.

XX 29-MAY-2003.

XX 16-AUG-2002; 2002US-00223085.

XX 20-JUN-2001; 2001WO-US019692.

PR 09-JUL-2001; 2001WO-US021735.

PR 20-FEB-2002; 2002US-00081056.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski RJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;

PI Watanabe CK, Williams PM, Wood WI, Ye W;

DR WPI; 2004-008957/01.

DR P-PSDB; ADE41266.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or PRO214, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and for treating disorders involving angiogenesis.

PS Claim 2; SEQ ID NO 15; 492pp; English.

XX The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial cell growth in a mammal. PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis. A PRO polypeptide, given in the specification, or an agonist is used to stimulate or inhibit smooth muscle cell growth, or an agonist is used to cell tube formation. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.

XX Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 86.5%; Score 1468.4; DB 12; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCCGGCGAGTCTGAAGATGGCCAATTACCGCTGGCACCAGAGATGA 288

Db 1 GAGCTCAGCCAGTGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACCAGAGATGA 60
QY 289 ATATGATGTCTCATAGAGGTCAACTGGAGAGCGATGAGCGAGCAATGTGCAAGTA 348
Db 61 ATATGATGTCTCATAGAGGTCAACTGGAGAGCGATGAGCGAGCAATGTGCAAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCAGCTCTGCTGTGTGTTGTGAT 408
Db 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCAGCTCTGCTGTGTGTTGTGAT 180
QY 409 CGGTGTCTGGACAATCTCTGTTGTGTTATCTCTGTTATCTCTGTTAAATATAAGGACTCAACG 468
Db 181 CGGTGTCTGGACAATCTCTGTTGTGTTATCTCTGTTAAATATAAGGACTCAACG 240
QY 469 CGTGGAAAATATCTATCTCTAACTTGGCAGTTTCTAACTCTGTTTCTTGTCTTACCCT 528
Db 241 CGTGGAAAATATCTATCTCTAACTTGGCAGTTTCTAACTCTGTTTCTTGTCTTACCCT 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAGGTAAGTCTAGT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAGGTAAGTCTAGT 420
QY 649 GTTTTGTGCAAGGGCACTTTTCTCAGCCAGGAGGGTGCCCTGTGGCATCATTTAC 708
Db 421 GTTTTGTGCAAGGGCACTTTTCTCAGCCAGGAGGGTGCCCTGTGGCATCATTTAC 480
QY 709 AAGTGTCTGGCATGGTAAACAGCCATTTCTGGCCACTTTGGCTGAATAGTGTGTTTATAA 768
Db 481 AAGTGTCTGGCATGGTAAACAGCCATTTCTGGCCACTTTGGCTGAATAGTGTGTTTATAA 540
QY 769 ACCTAGATGGAAGACAGAAATATAAGTGTGCATTTAGCAGAACTCCCTTCTGCGCAGC 828
Db 541 ACCTAGATGGAAGACAGAAATATAAGTGTGCATTTAGCAGAACTCCCTTCTGCGCAGC 600
QY 829 TGATGAGACATTTCTGAAGCATTTTCTGACTTTTAAATGAACTTTGGTCTGTTGCT 888
Db 601 TGATGAGACATTTCTGAAGCATTTTCTGACTTTTAAATGAACTTTGGTCTGTTGCT 660
QY 889 CCCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAACAACTAAGTTTCAGGGA 948
Db 661 CCCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAACAACTAAGTTTCAGGGA 720
QY 949 GCAGAGGTATAGCTTTTCAAGCTTTTGGCCATAATGGTAGTCTTCTTCTGATGTG 1008
Db 721 GCAGAGGTATAGCTTTTCAAGCTTTTGGCCATAATGGTAGTCTTCTTCTGATGTG 780
QY 1009 GGGCGCTACATATTTGCAATTTTCTGTCCTGTCCTTCAAGAACACTTCTCCCTGAGTGA 1068
Db 781 GGGCGCTACATATTTGCAATTTTCTGTCCTTCAAGAACACTTCTCCCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAACTCTGGCAAAAAGTGTTCACATCACTAACTCATCGCCACCAC 1128
Db 841 CTGCAAGAGCAGCTACAACTCTGGCAAAAAGTGTTCACATCACTAACTCATCGCCACCAC 900
QY 1129 CCACTGTGTCATCAACCTCTCTCTGTATGCGTTTCTGTATGGGACATTTAGCAAAATACCT 1188
Db 901 CCACTGTGTCATCAACCTCTCTCTGTATGCGTTTCTGTATGGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGCTGTTTCCATCTGCTAGTAAACACCCCACTTCAAGAACACTTCTCCCTGAGTGA 1248
Db 961 CTGCGCTGTTTCCATCTGCTAGTAAACACCCCACTTCAAGAACACTTCTCCCTGAGTGA 1020
QY 1249 AGGCACATCGAGGAGAACCTTGACCATTTCCACCGAAGTGAACCTAGCATCCACCAAT 1308
Db 1021 AGGCACATCGAGGAGAACCTTGACCATTTCCACCGAAGTGAACCTAGCATCCACCAAT 1080
QY 1309 GCAAGAAGATAAACAATGGAATTTTCTCTGCAATTTTCTGCAATTTTCTGCAATTTTCTACAC 1368

Db 1081 GCAAGAAGATAAACAATGGAATTTTCTCTGCAATTTTCTGCAATTTTCTACAC 1140
QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGTGAAGCTAAACATTTTGTAAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGTGAAGCTAAACATTTTGTAAAGC 1200
QY 1429 ACTGAATTTGTCTCAGGCAACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCCGCTCTCT 1488
Db 1201 ACTGAATTTGTCTCAGGCAACCGTGCAAGGCTCTTTTACAAACGTGAGCTCTTCCGCTCTCT 1260
QY 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGCG 1548
Db 1261 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGCG 1320
QY 1549 CGGAATTTGTCTAAGATCACTTAACTAGGAAGTGCAGAACTGATTCTCCAGCCCTGGT 1608
Db 1321 CGGAATTTGTCTAAGATCACTTAACTAGGAAGTGCAGAACTGATTCTCCAGCCCTGGT 1380
QY 1609 AGCATTTGTCTCAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTTGGGACAA 1668
Db 1381 AGCATTTGTCTCAGAGCTACGCTTGGTCCAGAACATCAAACTCCAAACCTTGGGACAA 1440
QY 1669 CGACATGAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAATAAATGATTTTAAACATC 1470

RESULT 9
ADH43448
ID ADH43448 standard; cDNA; 1475 BP.
XX
AC ADH43448;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human PRO polynucleotide #8.
XX
KW Human; PRO; gene; ss; cardiovascular disorder; endothelial disorder;
angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
cell apoptosis; cell tube formation; angiogenesis;
smooth muscle cell growth; myocardial infarction; trauma; cancer;
age-related macular degeneration; cytostatic; cardiant;
cerebroprotective; ophthalmological; vulnery.
XX
OS Homo sapiens.
XX
PN US2003224984-A1.
XX
PD 04-DEC-2003.
XX
PF 26-NOV-2002; 2002US-00305654.
XX
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritson ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pen J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;
XX
DR WPI; 2004-042166/04.
XX
PS P-PSDB; ADH43449.
XX
PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
or age-related macular degeneration.
XX
PS Claim 2; SEQ ID NO 15; 492pp; English.
XX
CC The invention relates to human PRO polypeptides and the PRO
polynucleotides encoding them. The invention also relates to treating
cardiovascular, endothelial or angiogenic disorders in mammals,
inhibiting endothelial cell growth, stimulating endothelial cell growth,

CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
CC polynucleotide of the invention.

XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
Query Match 86.5%; Score 1468.4; DB 12; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	229	GGAGCTCAGCCAGTGGGCGAGTCTGAGATGGCCAAATTACAGCTGGCCACGAGAGATGA	288
DB	1	GGAGCTCAGCCAGTGGGCGAGTCTGAGATGGCCAAATTACAGCTGGCCACGAGAGATGA	60
QY	289	ATATGATGTCTCATAGAAGGTGAATCGAGAGCGATGAGGAGCAATGTGCAAGTA	348
DB	61	ATATGATGTCTCATAGAAGGTGAATCGAGAGCGATGAGGAGCAATGTGCAAGTA	120
QY	349	TGAGCCGAGGCACTCTCAGCCAGCTGGTGCCATCATCTCTCTGCTGTGTTGTGAT	408
DB	121	TGAGCCGAGGCACTCTCAGCCAGCTGGTGCCATCATCTCTCTGCTGTGTTGTGAT	180
QY	409	CGGTGCTCTGGCAATCTCTCGTGTGCTTATCTCTGTTAAATATGAAGACTCAACG	468
DB	181	CGGTGCTCTGGCAATCTCTCGTGTGCTTATCTCTGTTAAATATGAAGACTCAACG	240
QY	469	CGTGGAAATATCTATCTTAAACTTGGCAGTCTTAACTTGTGTCTTCTTACCT	528
DB	241	CGTGGAAATATCTATCTTAAACTTGGCAGTCTTAACTTGTGTCTTCTTACCT	300
QY	529	GCCTTCTGGGCTCATGTGGGGGGATCCCATGTGTAATAATCTCATTTGGACTGATTT	588
DB	301	GCCTTCTGGGCTCATGTGGGGGGATCCCATGTGTAATAATCTCATTTGGACTGATTT	360
QY	589	CGTGGGCTCATGTGAGACATTTTCAATTTGCTCTGACTGTGCAAGGTACTAGT	648
DB	361	CGTGGGCTCATGTGAGACATTTTCAATTTGCTCTGACTGTGCAAGGTACTAGT	420
QY	649	GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCTTGGCATCATTTAC	708
DB	421	GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGGGTGCTTGGCATCATTTAC	480
QY	709	AAGTGTCTGGCATGGTAAACAGCCATCTTGCCCACTTTTGGCTGAATACGTGGTTATAA	768
DB	481	AAGTGTCTGGCATGGTAAACAGCCATCTTGCCCACTTTTGGCTGAATACGTGGTTATAA	540
QY	769	ACCTCAGATGGAGACCAAGATACAGTGTGCAATTTAGCAGAACTCCCTTCTCCGACG	828
DB	541	ACCTCAGATGGAGACCAAGATACAGTGTGCAATTTAGCAGAACTCCCTTCTCCGACG	600
QY	829	TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTGGTTCCT	888
DB	601	TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTGGTTCCT	660
QY	889	CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGTTTCAGGA	948
DB	661	CCCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAACACATAAGTTTCAGGA	720
QY	949	CGAGAGGTATAGCTTTTCAAGCTTTTTCGCTAATAGGTAGTCTTCTCTCTGATGTG	1008
DB	721	CGAGAGGTATAGCTTTTCAAGCTTTTTCGCTAATAGGTAGTCTTCTCTCTGATGTG	780
QY	1009	GGCGCCCTACAATATTGCAATTTTCTCTGTCCTTCAAGAACACTTCTCTCCCTGAGTGA	1068

DB	781	GGCGCCCTACAATATTGCAATTTTCTCTGTCCTCACTTTTCAAGAACACTTCTCTCCCTGAGTGA	840
QY	1069	CTGCAAGAGCAGCTACAATCTGGAACAAAGTGTTCACATCACTAACTCATCGCCACCAC	1128
DB	841	CTGCAAGAGCAGCTACAATCTGGAACAAAGTGTTCACATCACTAACTCATCGCCACCAC	900
QY	1129	CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCT	1188
DB	901	CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCT	960
QY	1189	CTGCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACA	1248
DB	961	CTGCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACA	1020
QY	1249	AGGCACATCGAGGGAAGAACCTCGACCATTCACCGAAGTGTAACTAGCATCCACAAT	1308
DB	1021	AGGCACATCGAGGGAAGAACCTCGACCATTCACCGAAGTGTAACTAGCATCCACAAT	1080
QY	1309	GCAAGAACATAAATCATGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC	1368
DB	1081	GCAAGAACATAAATCATGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC	1140
QY	1369	ATTTGTATACAAATTCGGATACAGGAAGAAAGGAGAGGTGAGCTAACTTTGCTAAGC	1428
DB	1141	ATTTGTATACAAATTCGGATACAGGAAGAAAGGAGAGGTGAGCTAACTTTGCTAAGC	1200
QY	1429	ACTGAATTTGCTCAGGCACCGTGCAGGCTCTTTTACAAACGTGAGCTCTTCGCTCTCT	1488
DB	1201	ACTGAATTTGCTCAGGCACCGTGCAGGCTCTTTTACAAACGTGAGCTCTTCGCTCTCT	1260
QY	1489	ACCCTTCTCATAGTGTGGATAGGACTAGTCTCATTTTCTGAGAAGAAACTAAGGCG	1548
DB	1261	ACCCTTCTCATAGTGTGGATAGGACTAGTCTCATTTTCTGAGAAGAAACTAAGGCG	1320
QY	1549	CGGAAATTTGCTTAAGATCATTAACTAGGAAGTGGCAGAACTGATTTCCAGCCCTGGT	1608
DB	1321	CGGAAATTTGCTTAAGATCATTAACTAGGAAGTGGCAGAACTGATTTCCAGCCCTGGT	1380
QY	1609	AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGGACAAA	1668
DB	1381	AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGGACAAA	1440
QY	1669	CGCATGAAATAAATGTAATTTTAAACATC	1698
DB	1441	CGCATGAAATAAATGTAATTTTAAACATC	1470

RESULT 10

ADK82793

ID ADK82793 standard; cDNA; 1475 BP.

XX

AC ADK82793;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human PRO polynucleotide #8.

XX

Human; PRO; gene; 86; cardiovascular disorder; endothelial disorder;
angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
cell apoptosis; cell tube formation; angiogenesis;
smooth muscle cell growth; myocardial infarction; trauma; cancer;
age-related macular degeneration; cytostatic; cardiant;
cerebroprotective; ophthalmological; vulnery.

OS Homo sapiens.

XX

PN US2004043927-A1.

XX

PD 04-MAR-2004.

XX

PF 20-FEB-2002; 2002US-00081056.

XX

PR 19-SEP-1997; 97US-00933821.

PR	29-JAN-1998;	98US-00015089.	PR	01-MAR-2001;	2001WO-US006666.
PR	10-SEP-1998;	98WO-US018624.	PR	09-MAR-2001;	2001US-00802706.
PR	14-SEP-1998;	98WO-US019177.	PR	14-MAR-2001;	2001US-00808689.
PR	16-SEP-1998;	98WO-US019330.	PR	05-APR-2001;	2001US-00828366.
PR	17-SEP-1998;	98WO-US019437.	PR	25-MAY-2001;	2001US-00866028.
PR	19-NOV-1998;	98US-00180997.	PR	25-MAY-2001;	2001US-00866034.
PR	01-DEC-1998;	98WO-US025108.	PR	25-MAY-2001;	2001WO-US017092.
PR	22-DEC-1998;	98US-00218517.	PR	01-JUN-2001;	2001US-00872035.
PR	03-JAN-1999;	99WO-US0000106.	PR	01-JUN-2001;	2001WO-US017800.
PR	12-FEB-1999;	99US-00214186.	PR	14-JUN-2001;	2001US-00882636.
PR	08-MAR-1999;	99US-00254311.	PR	19-JUN-2001;	2001US-00886342.
PR	03-MAR-1999;	99WO-US005028.	PR	20-JUN-2001;	2001US-00891692.
PR	09-MAR-1999;	99US-00254460.	PR	29-JUN-2001;	2001WO-US019692.
PR	12-MAR-1999;	99US-00267213.	PR	09-JUL-2001;	2001WO-US021066.
PR	13-APR-1999;	99US-00284291.	PR	30-JUL-2001;	2001US-00918585.
PR	02-JUN-1999;	99WO-US013252.	PR	06-AUG-2001;	2001US-00924419.
PR	14-JUN-1999;	99US-00332928.	PR	09-AUG-2001;	2001US-00927796.
PR	14-JUN-1999;	99US-00380137.	PR	13-AUG-2001;	2001US-00929404.
PR	25-AUG-1999;	99US-00380138.	PR	16-AUG-2001;	2001US-00931836.
PR	23-AUG-1999;	99US-00380139.	PR	28-AUG-2001;	2001US-00941992.
PR	01-SEP-1999;	99WO-US020111.	PR	04-SEP-2001;	2001US-00946374.
PR	08-SEP-1999;	99WO-US020594.	PR	07-SEP-2001;	2001US-00948901.
PR	13-SEP-1999;	99WO-US020944.	PR	15-NOV-2001;	2001US-00002796.
PR	15-SEP-1999;	99WO-US021090.	PR	30-NOV-2001;	2001US-00001054.
PR	15-SEP-1999;	99WO-US021547.	PR	06-DEC-2001;	2001US-00008667.
PR	03-OCT-1999;	99WO-US023089.	PR	19-DEC-2001;	2001US-00028072.
PR	15-OCT-1999;	99US-00403154.	PR	15-JAN-2002;	2002US-00052586.
PR	18-OCT-1999;	99US-00403296.	PR	17-JAN-2002;	2002US-00053107.
PR	18-OCT-1999;	99US-00403297.	PR	18-JAN-2002;	2002US-00053594.
PR	10-NOV-1999;	99US-00423741.	PR	08-FEB-2002;	2002US-00072068.
PR	12-NOV-1999;	99US-00423843.	PR	09-APR-2002;	2002US-00119480.
PR	13-NOV-1999;	99US-00423844.	XX		
PR	29-NOV-1999;	99WO-US028214.	PA	(GETH) GENENTECH INC.	
PR	30-NOV-1999;	99WO-US028313.	XX		
PR	01-DEC-1999;	99WO-US028301.	PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;	
PR	01-DEC-1999;	99WO-US028634.	PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JP;	
PR	02-DEC-1999;	99WO-US028551.	PI	Watanabe CK, Williams PM, Wood WI, Ye W;	
PR	02-DEC-1999;	99WO-US028564.	XX		
PR	02-DEC-1999;	99WO-US028565.	DR	WPI; 2004-225727/21.	
PR	16-DEC-1999;	99WO-US030095.	DR	P-PSDB; ADK82794.	
PR	20-DEC-1999;	99WO-US030999.	XX		
PR	30-DEC-1999;	99WO-US031243.	XX		
PR	30-DEC-1999;	99WO-US031274.	FT	New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or	
PR	05-JAN-2000;	2000WO-US000219.	FT	PRO21383, useful in molecular biology, chromosome and gene mapping, in	
PR	06-JAN-2000;	2000WO-US000376.	XX	generating antisense RNA and DNA, and in gene therapy.	
PR	11-FEB-2000;	2000WO-US003565.	PS	Claim 2; SEQ ID NO 15; 494pp; English.	
PR	18-FEB-2000;	2000WO-US004341.	XX		
PR	18-FEB-2000;	2000WO-US004342.	CC	The invention relates to human PRO polypeptides and the PRO	
PR	22-FEB-2000;	2000WO-US004414.	CC	polynucleotides encoding them. The invention also relates to treating	
PR	24-FEB-2000;	2000WO-US004914.	CC	cardiovascular, endothelial or angiogenic disorders in mammals,	
PR	24-FEB-2000;	2000WO-US005004.	CC	inhibiting endothelial cell growth, stimulating endothelial cell growth,	
PR	01-MAR-2000;	2000WO-US0050601.	CC	inducing cardiac hypertrophy, cell apoptosis or cell tube formation and	
PR	02-MAR-2000;	2000WO-US005841.	CC	stimulating angiogenesis or smooth muscle cell growth by administering	
PR	10-MAR-2000;	2000WO-US006319.	CC	polypeptides of the invention. The PRO polypeptides and polynucleotides	
PR	15-MAR-2000;	2000WO-US006884.	CC	are useful for treating cardiovascular, endothelial or angiogenic	
PR	20-MAR-2000;	2000WO-US007377.	CC	disorders, e.g. myocardial inf	

[illegible]

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP3619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42969 encode GPCR proteins given in ABP1675 to ABP82018, which are used in the exemplification of the present invention

Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other:

Qy	239	CCAGTGGG	CAGTCTGA	AGATGGCC	CAATTAC	AGCTGG	CGCACAG	GAGGATGA	TATGATGC	298	
Db	185	CCA	CAGGCG	CAGTCTGA	AGATGGCC	CAATTAC	AGCTGG	CGCACAG	GAGGATGA	TATGATGC	244
Qy	299	CTCATAGA	AGGTGA	AACTGG	GAGCGAT	GAGCG	CAGCAAT	GTGCA	AGTATG	ACGCCCAG	358
Db	245	CTCATAGA	AGGTGA	AACTGG	GAGCGAT	GAGCG	CAGCAAT	GTGCA	AGTATG	ACGCCCAG	304
Qy	359	GCACTCTC	CAGCCC	AGCTGG	TGCCATCA	CTCTG	CTGCTGT	GTGTGT	TGTGAT	CGGTGTCGTG	418
Db	305	GCACTCTC	CAGCCC	AGCTGG	TGCCATCA	CTCTG	CTGCTGT	GTGTGT	TGTGAT	CGGTGTCGTG	364
Qy	419	GACAACTC	TCTCGT	TGTGCTTAT	CCTGGT	TAAATAT	AAAGACT	CAAA	CGGTGG	AAAT	478
Db	365	GACAACTC	TCTCGT	TGTGCTTAT	CCTGGT	TAAATAT	AAAGACT	CAAA	CGGTGG	AAAT	424
Qy	479	ATCTATCT	TCTTAA	ACTTTGG	CGAGTTTCT	TAACTTGT	TGTTTCT	TGCTTAC	CCCTGCC	CTTCGG	538
Db	425	ATCTATCT	TCTTAA	ACTTTGG	CGAGTTTCT	TAACTTGT	TGTTTCT	TGCTTAC	CCCTGCC	CTTCGG	484
Qy	539	GCTCATG	TCTGGG	GCGATCC	CAATGTG	TAAATAT	TCTCAT	TGAC	TGTACTT	CGTGGGCGTG	598
Db	485	GCTCATG	TCTGGG	GCGATCC	CAATGTG	TAAATAT	TCTCAT	TGAC	TGTACTT	CGTGGGCGTG	544
Qy	599	TACAGT	GAGACAT	TTTTTCA	ATTGCTT	CTGACT	GTGCA	AAAGGTAC	TAGTGT	TTTTTGCAC	658
Db	545	TACAGT	GAGACAT	TTTTTCA	ATTGCTT	CTGACT	GTGCA	AAAGGTAC	TAGTGT	TTTTTGCAC	604
Qy	659	AAGGGCAA	CTTTTTTCT	CAGCC	GAGGAGG	GTGCCCTGTG	GCATCAT	TATTACA	AGTGTCTCGT	718	
Db	605	AAGGGCAA	CTTTTTTCT	CAGCC	GAGGAGG	GTGCCCTGTG	GCATCAT	TATTACA	AGTGTCTCGT	664	
Qy	719	GCATGGGT	TACAG	GCATTTCTG	GCACATTG	GCTGAA	TACGTGG	TTTTTATA	AAACCTC	CAGATG	778
Db	665	GCATGGGT	TACAG	GCATTTCTG	GCACATTG	GCTGAA	TACGTGG	TTTTTATA	AAACCTC	CAGATG	724
Qy	779	GAAGAC	CAGAAATACA	AGTGTG	CAATTAG	CAGAACTCC	CTTCC	TGCGC	AGCTGAT	GAGACA	838
Db	725	GAAGAC	CAGAAATACA	AGTGTG	CAATTAG	CAGAACTCC	CTTCC	TGCGC	AGCTGAT	GAGACA	784
Qy	839	TTCTCG	GAGCA	TTTTTCT	GACTTTTAAAA	TGAAC	ATTTTGG	TTTTTCTG	TGCTCC	CTCCCTATTT	898

RESULT 12

ADN95729

ADN95729
ID ADN95729 standard; DNA; 1645 BP.

AC ADN95729;

01-JUL-2004 (first entry)

XX
DE Human BEC/LEC-related gene sequence SeqID653.

growth; differentiation; blood endothelial cell; BEC;

KW growth; differentiation; blood endothelial cell; BEC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;

KW lymphatic endothelial cell; LEC, leucocytic lymphoedema; VEGF-C, lymphatic growth agent; VEGF-D, antiangiogenic; cytostatic; KW lymphatic growth agent; VEGF-C; VEGF-D

785 TTCTGGAAGCATTTTCTCTGACTTTTAAATAATGAACATTTTCCGTTCTTGCTCTCCCTCCCTATTTT 844

899 ATTTTTCACATTTTCTCTATGTGCAATATGAGAAACACATTAAGTGTTCAGGAGCAGAGGTAT 958

845 ATTTTTCACATTTTCTCTATGTGCAATATGAGAAACACATTAAGTGTTCAGGAGCAGAGGTAT 904

959 AGCCTTTTCAAGCTGTGTTTTCGCCATAATGGTGTCTTCTTCTGATGTGGGGCCCTAC 1018

905 AGCCTTTTCAAGCTGTGTTTTCGCCATAATGGTGTCTTCTTCTGATGTGGGGCCCTAC 964

1019 AATATTGCATTTTTCCTGTGCCATTTTCAAGGAACACTTCTCCCTGAGTGACTGCAAGAGC 1078

965 AATATTGCATTTTTCCTGTGCCATTTTCAAGGAACACTTCTCCCTGAGTGACTGCAAGAGC 1024

1079 AGCTACCAATCTGGACAAAAGTGTTCACATCATCTAACTCATCTGCACACACCCACTGCTGC 1138

1025 AGCTACCAATCTGGACAAAAGTGTTCACATCATCTAACTCATCTGCACACACCCACTGCTGC 1084

1139 ATCAACCCCTCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCGTGT 1198

1085 ATCAACCCCTCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCGTGT 1144

1199 TTCCATCTGGGTAGTAACACCCCATCTCAACCCAGGGGGCAGTCTGCACAAAGGCACATCG 1258

1145 TTCCATCTGGGTAGTAACACCCCATCTCAACCCAGGGGGCAGTCTGCACAAAGGCACATCG 1204

1259 AGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCTCACCAATGCAAGAGAA 1318

1205 AGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCTCACCAATGCAAGAGAA 1264

1319 TAAACATGGATTTTTCATCTTTCTGCAATTTATTCATGTAAATTTTCTACATTTGTATAC 1378

1265 TAAACATGGATTTTTCATCTTTCTGCAATTTATTCATGTAAATTTTCTACATTTGTATAC 1324

1379 AAATTCGATACAGGAAGAAAGGAGAGGTGTAGCTAACTTTGCTTAAGCACTGCAATTTG 1438

1325 AAATTCGATACAGGAAGAAAGGAGAGGTGTAGCTAACTTTGCTTAAGCACTGCAATTTG 1384

1439 TCTCAGGCACCGTGCAAGGCTCTTTTACAAAGGTGTAGCTTCCCTTCCTTACCACCTTGTCTC 1498

1385 TCTCAGGCACCGTGCAAGGCTCTTTTACAAAGGTGTAGCTTCCCTTCCTTACCACCTTGTCTC 1444

1499 CATAGTGTGGATGAGCTAGTCTCATTTTCTCTGAGAAAGAAATTAAGGCGCGGAAATTTG 1558

1445 CATAGTGTGGATGAGCTAGTCTCATTTTCTCTGAGAAAGAAATTAAGGCGCGGAAATTTG 1504

1559 TCTTAAGTACATTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGTAGCATTTGCT 1618

1505 TCTTAAGTACATTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGTAGCATTTGCT 1564

1619 CAGAGCCTACGCTTGGTCCAGAACTCAAACTCCAAACCCCTGGGGGCAAAACGACATGAAA 1678

1565 CAGAGCCTACGCTTGGTCCAGAACTCAAACTCCAAACCCCTGGGGGCAAAACGACATGAAA 1624

1679 TAAATGTATTTTAAACATC 1698

1625 TAAATGTATTTTAAACATC 1644

XX
DE Human BEC/LEC-related gene sequence SeqID653.

KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
XX human.
XX Homo sapiens.
OS WO2003080640-A1.
XX 02-OCT-2003.
XX 07-MAR-2003; 2003WO-US006900.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
PI Aitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI: 2003-876899/81.
DR P-PSDB; ADN95728.
XX
PS Example 1; SEQ ID NO 653; 176pp; English.
XX
CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprises contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
CC composition comprising a lymphatic growth agent selected from VEGF-C or
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC the development of compounds with an antiangiogenic, cytostatic,
CC vasotropic or antiinflammatory activity or for gene therapy. The method
CC is useful in modulating the growth or differentiation of blood
CC endothelial cells or lymphatic endothelial cells, in treating hereditary
CC lymphoedema, in screening for an endothelial cell disorder or
CC predisposition to the disorder or in monitoring the efficacy or toxicity
CC of a drug on endothelial cells. The agent is useful in manufacturing a
CC medicament for the differential modulation of blood vessel endothelial
CC cell or lymphatic vessel endothelial cell growth or differentiation. The
CC lymphatic growth agent may also be used in manufacturing a medicament for
CC the treatment of hereditary lymphoedema resulting from a mutation in a
CC LEC gene or of other diseases involving the lymphatic vessels, such as
CC various inflammatory diseases and cancer metastasis via the lymphatic
CC system. The present sequence is that of a human LEC/BEC differentially
CC expressed gene which is related to the method of the invention. Note: This
CC sequence does not appear in the specification but was obtained by the
CC indexer using the source data given in table 14 of the specification.
XX
SQ Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other;

Query Match 85.7%; Score 1455.2; DB 11; Length 1645;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 239 CCAGTGGGCGAGTCTGAAGATGGCCAAATTACAGCTGGCACCGAGGATGAATATGATGTC 298
DB 185 CCACAGGGCGAGTCTGAAGATGGCCAAATTACAGCTGGCACCGAGGATGAATATGATGTC 244
QY 299 CTCATAGAAGGTGAACCTGAGAGCGATGAGGAGAGCAATGTGAACAGTATGACGCCAG 358
DB 245 CTCATAGAAGGTGAACCTGAGAGCGATGAGGAGAGCAATGTGAACAGTATGACGCCAG 304
QY 359 GCACTCTGAGCCGAGCTGGTGCATCACCTGCTGCTGCTGTTGTTGATCGGTGCTCG 418
DB 305 GCACTCTGAGCCGAGCTGGTGCATCACCTGCTGCTGCTGTTGTTGATCGGTGCTCG 364
QY 419 GACAATCTCCTGGTGTGCTTATCTCGTGGTAAATATAAAGGACTCAAACCGCTGGAAAT 478

DB 365 GACAATCTCCTGGTGTGCTTATCTCGTGGTAAATATAAAGGACTCAAACCGCTGGAAAT 424
QY 479 ATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTTGTTTCTTGTCTTACCTGCGCTCTGG 538
DB 425 ATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTTGTTTCTTGTCTTACCTGCGCTCTGG 484
QY 539 GCTCATGCTGGGGGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTTGGGCTG 598
DB 485 GCTCATGCTGGGGGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTTGGGCTG 544
QY 599 TACAGTGAGACATTTTTCATTTGCCCTTCTGACTGTGCAAGAGTACTAGTGTGTTTGCAC 658
DB 545 TACAGTGAGACATTTTTCATTTGCCCTTCTGACTGTGCAAGAGTACTAGTGTGTTTGCAC 604
QY 659 AAGGCAACTTTTCTCAGCCAGGAGGGTGGCTGTGCGCATCATTTACAAGTGTCTG 718
DB 605 AAGGCAACTTTTCTCAGCCAGGAGGGTGGCTGTGCGCATCATTTACAAGTGTCTG 664
QY 719 GCATGGGTAAACAGCCATTTCTGGCCACTTTGCTCTGAATACGTGGTTTATAAACCTCAGATG 778
DB 665 GCATGGGTAAACAGCCATTTCTGGCCACTTTGCTCTGAATACGTGGTTTATAAACCTCAGATG 724
QY 779 GAAGACCAGAAATACAACTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACA 838
DB 725 GAAGACCAGAAATACAACTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACA 784
QY 839 TTCTGGAGACATTTTCTGACTTTTAAATGACATTTTGGTTCTTGTCTCTCCCTCTTTT 898
DB 785 TTCTGGAGACATTTTCTGACTTTTAAATGACATTTTGGTTCTTGTCTCTCCCTCTTTT 844
QY 899 ATTTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGTAT 958
DB 845 ATTTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGTAT 904
QY 959 AGCCTTTTCAAGCTTTGTTTGGCCATAATGTFAGTCTTCTTCTGATGTGGGGCCCTTAC 1018
DB 905 AGCCTTTTCAAGCTTTGTTTGGCCATAATGTFAGTCTTCTTCTGATGTGGGGCCCTTAC 964
QY 1019 AATATTGATTTTCTCTGCTCCACTTTTCAAGAACACTTTCTCCCTGAGTGACTGCAAGAGC 1078
DB 965 AATATTGATTTTCTCTGCTCCACTTTTCAAGAACACTTTCTCCCTGAGTGACTGCAAGAGC 1024
QY 1079 AGCTACAATCTGGACAAAAAGTTTCACTCACTAACTCATCGCCACCACCCACTGCTGC 1138
DB 1025 AGCTACAATCTGGACAAAAAGTTTCACTCACTAACTCATCGCCACCACCCACTGCTGC 1084
QY 1139 ATCAACCTCTCTGATGTGCTGTTTCTGATGGGACATTTAGCAATACTCTGTCGCGCTGT 1198
DB 1085 ATCAACCTCTCTGATGTGCTGTTTCTGATGGGACATTTAGCAATACTCTGTCGCGCTGT 1144
QY 1199 TTCCATCTGCGTAGTAACACCCCTTCAACCCAGGGGCGAGTCTGCAACAGGCACATCG 1258
DB 1145 TTCCATCTGCGTAGTAACACCCCTTCAACCCAGGGGCGAGTCTGCAACAGGCACATCG 1204
QY 1259 AGGGAAGAACTGACCATTTCCACCAGAGTGTAAACTAGCATCCACCAATGCAAGAGAA 1318
DB 1205 AGGGAAGAACTGACCATTTCCACCAGAGTGTAAACTAGCATCCACCAATGCAAGAGAA 1264
QY 1319 TAAACATGGATTTTCATCTTTCTGATTAATTTTCATGTAATTTTCTACATTTGTATAC 1378
DB 1265 TAAACATGGATTTTCATCTTTCTGATTAATTTTCATGTAATTTTCTACATTTGTATAC 1324
QY 1379 AAAATCGGATACAGGAAGAAAGGAGGTGAGCTTACATTTGCTTACGACTGAAATTTG 1438
DB 1325 AAAATCGGATACAGGAAGAAAGGAGGTGAGCTTACATTTGCTTACGACTGAAATTTG 1384
QY 1439 TCTCAGGCACCGTGCAGAGCTCTTTTACAAAAGTGTAGCTCTTTCGCTCTCTACCATTTGTC 1498
DB 1385 TCTCAGGCACCGTGCAGAGCTCTTTTACAAAAGTGTAGCTCTTTCGCTCTCTACCATTTGTC 1444
QY 1499 CATAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAGAAACTAAGGGCGGGAATTTG 1558
DB 1445 CATAGTGTGATAGGACTAGTCTCATTTCTCTGAGAGAGAAACTAAGGGCGGGAATTTG 1504

Db 725 GAAGACAGAAATACAAGTGTGATTTAGCAGAACTCCCTTCCTGCCAGCTGATGACAA 784
QY TTCTGGAGCATTTTCTGACTTTTAAATAAGCAATTTTCGTTCTTCCTCCCTATTT 898
Db 785 TTCTGGAGCATTTTCTGACTTTTAAATAAGCAATTTTCGTTCTTCCTCCCTATTT 844
QY ATTTTACATTTCTTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGTAT 958
Db 845 ATTTTACATTTCTTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGTAT 904
QY AGCTTTTCAAGCTTGTGTTTTCGCAATATGTTAGTCTTCTTCCTGATGTGGCGCCCTAC 1018
Db 905 AGCTTTTCAAGCTTGTGTTTTCGCAATATGTTAGTCTTCTTCCTGATGTGGCGCCCTAC 964
QY AATATTGCAATTTTCTGTGCTCCACTTTTCAAGAAACACTTTCTCCCTGAGTGAAGTCAAGAGC 1078
Db 965 AATATTGCAATTTTCTGTGCTCCACTTTTCAAGAAACACTTTCTCCCTGAGTGAAGTCAAGAGC 1024
QY AGCTACAATCTGACAAAAGTGTTCACATCACTAATCTCATCGCCACCCACTGCTGC 1138
Db 1025 AGCTACAATCTGACAAAAGTGTTCACATCACTAATCTCATCGCCACCCACTGCTGC 1084
QY ATCAACCCCTCTCTGTATGCTTTCTTGTGAGGACATTTAGCAAAATACCTCTGCCCTGT 1198
Db 1085 ATCAACCCCTCTCTGTATGCTTTCTTGTGAGGACATTTAGCAAAATACCTCTGCCCTGT 1144
QY TTCATCTGGTGTAGTAACACCCACTTCAACCCAGGGGAGTCTGCACAAAGCACAATCG 1258
Db 1145 TTCATCTGGTGTAGTAACACCCACTTCAACCCAGGGGAGTCTGCACAAAGCACAATCG 1204
QY AGGGAAGAACTGACCACTTCCACCGAAGTGAATAGCATCCACCAATGCAAGAGAA 1318
Db 1205 AGGGAAGAACTGACCACTTCCACCGAAGTGAATAGCATCCACCAATGCAAGAGAA 1264
QY TAAACATGATTTTCTATCTTCTGCAATTTTCAATGTAATTTTCTACATTTGTATAC 1378
Db 1265 TAAACATGATTTTCTATCTTCTGCAATTTTCAATGTAATTTTCTACATTTGTATAC 1324
QY AAATCGGATACAGGAAGAAAGGAGAGTGAAGTGAATTTGCTAAGCACTGAATTTG 1438
Db 1325 AAATCGGATACAGGAAGAAAGGAGAGTGAAGTGAATTTGCTAAGCACTGAATTTG 1384
QY TCTCAGGACCGTGAAGGCTTTTCAAAAGTGAAGTGAATTTGCTAAGCACTGAATTTG 1498
Db 1385 TCTCAGGACCGTGAAGGCTTTTCAAAAGTGAAGTGAATTTGCTAAGCACTGAATTTG 1444
QY CATAGTGTGATAGGACTAGTCTCATTTCTCAGAGAAACTAAGGCGGGAATTTG 1558
Db 1445 CATAGTGTGATAGGACTAGTCTCATTTCTCAGAGAAACTAAGGCGGGAATTTG 1504
QY TCTAAGATCACTTAACCTAGGAAGTGCAGAACTGATTTCTCAGCCCTGGTGTAGCATTTGCT 1618
Db 1505 TCTAAGATCACTTAACCTAGGAAGTGCAGAACTGATTTCTCAGCCCTGGTGTAGCATTTGCT 1564
QY CAGAGCCTACGCTTGTGTCAGAACTCAAACTCCAAACCTCGGGGCAAAACGACATGAAA 1678
Db 1565 CAGAGCCTACGCTTGTGTCAGAACTCAAACTCCAAACCTCGGGGCAAAACGACATGAAA 1624
QY TAAATGATTTTAAACATC 1698
Db 1625 TAAATGATTTTAAACATC 1644

RESULT 15

ABD20648 ID ABD20648 standard; DNA; 143040 BP.

XX AC ABD20648;

XX AC ABD20648;

DT 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #259.

XX

Human; antitense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; da.
Homo sapiens.
WO200285309-A2.
31-OCT-2002.
23-APR-2002; 2002WO-US013143.
24-APR-2001; 2001US-0286036P.
(EPIG-) EPIGENESIS PHARM INC.
Nyce JW, Li Y, Sandraeagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S;
WPI; 2003-093058/08.
Pharmaceutical composition for treating asthma, has antitense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.
Claim 15; SEQ ID NO 12041; 763pp; English.
This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it

Sequence 143040 BP; 41190 A; 30113 C; 32394 G; 39343 T; 0 U; 0 Other;

Query Match 85.7%; Score 1455.2; DB 11; Length 143040;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 239 CCAGTGGGCGAGTCTGAAGATGCCCAATTACAGCTGGCAGGAGATGAATGATGTC 298

Db 96624 CCACAGGGCGAGTCTGAAGATGCCCAATTACAGCTGGCAGGAGATGAATGATGTC 96683

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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 14:53:56 ; Search time 5809 Seconds
(without alignments)
11126.378 Million cell updates/sec

Title: AF014958

Perfect score: 1698

Sequence: 1 AGACGGTTCAGAGATCCTCT.....TAAATGTATTTAAACATC 1698

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	779.8	45.9	831	4	BI834559 603089767
2	763	44.9	880	4	BI819787 603041489
3	737.8	43.5	896	5	BQ892457 AGENCOURT
4	689	40.6	729	6	CD370587 UI-H-FTL-
5	688.4	40.5	716	7	CF147784 AGENCOURT
6	681.8	40.2	750	2	BE871331 601449442
7	646.4	38.1	1035	4	BG386374 602435580
8	629	37.0	720	6	CD520843 AGENCOURT
9	597.6	35.2	773	7	CO959196 AGENCOURT
10	581	34.2	581	5	BP300486 BP300486
11	573.4	33.8	576	5	BP295805 BP295805
12	553.4	32.6	581	5	BP300273 BP300273
13	545.8	32.1	573	2	AW300833 xk06907.x
14	520.4	30.6	547	1	AI343408 tB9606.x
15	479	28.2	517	5	EX480211 DXFZp6861
16	469.8	27.7	475	2	BE465578 hu32605.x
17	462.2	27.2	2111	3	AK007808 Mus muscu
18	450.6	26.5	768	6	CD468404 LeukoS3_3
19	431.8	25.4	736	6	CD466140 LeukoS2_2
20	415.4	24.5	789	6	CD466479 LeukoN2_4
21	401	23.6	467	7	CR549318 DXFZp468A
22	398	23.4	683	6	CD535056 LeukoN5_3
23	396	23.3	424	2	AW293465 UI-H-BI2-
24	395.6	23.3	650	6	CD467795 LeukoS1_7

C	25	395.4	23.3	397	1	AI954582	AI954582 wx93902.x
	26	395	23.3	664	6	CD470054	LeukoS4_1
	27	394.8	23.3	673	6	CD466424	LeukoN2_4
	28	393.2	23.2	691	6	CD468594	LeukoS3_4
	29	391.8	23.1	654	6	CD466568	LeukoN2_7
	30	391.4	23.1	728	7	CO959203	AGENCOURT
	31	385	22.7	749	6	CD468632	LeukoS3_4
	32	382.6	22.5	724	6	CD469405	LeukoS2_3
	33	378.4	22.3	623	6	CD471186	LeukoS5_1
	34	375	22.1	702	6	CD468196	LeukoS3_1
	35	363.6	21.4	692	7	CN786392	4120380_B
	36	363	21.4	369	1	AI288845	qn24e01.x
	37	348.2	20.5	592	6	CD536762	LeukoN6_6
	38	345	20.3	592	6	CD471634	LeukoS6_4
	39	343.8	20.2	793	6	CD466229	LeukoN2_2
	40	341.6	20.1	578	6	CD465152	LeukoN1_2
	41	339.2	20.0	722	7	CK835230	4059514_B
	42	329.8	19.4	556	6	CD471194	LeukoS5_1
	43	329.8	19.4	564	6	CD467249	LeukoS1_3
	44	326.4	19.2	561	6	CD465288	LeukoN1_3
	45	325	19.1	564	6	CD472150	LeukoS6_1

ALIGNMENTS

BI834559 831 bp mRNA linear EST 04-OCT-2001
603089767F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228561 5',
mRNA sequence.

ACCESSION BI834559

VERSION BI834559.1 GI:15946109

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgc.ncl.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLM11575 row: f column: 18

High quality sequence stop: 813.

Location/Qualifiers

1..831

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/lab_host="DH10B"

/clone="IMAGE:5228561"

/clone_lib="NIH MGC 120"

/note="Organ: pooled pancreas and spleen; Vector:

pcMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of spleen and pancreas from 28 yo

male. Library is oligo-dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 1.5 kb, insert size range 1-2.5 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match

45.9%; Score 779.8; DB 4; Length 831;

Best Local Similarity 99.3%; Pred. No. 1.6e-216;		Matches 825; Conservative 0; Mismatches 2; Indels 4; Gaps 4;	
QY	64	CTGAGCTCGTGAAGTGGGGGGTGAAGCCACAGGGGAA-TCAACAGTGGTTCTCGTG	122
Db	1	CTGAGCTCGTGAAGTGGGGGGTGAAGCCACAGGTGAAGTCAACAGTGGTTCTCGTG	60
QY	123	CCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGGGATCCACATGTCGGGGCCATCCC	182
Db	61	CCCTCACA-GGT CAGGAGCAGTCTGATCAAAAGAGGGGATCCACATGTCGGGGCCATCCC	119
QY	183	CACAGCTCCCGGATGCTGGGTCTGAGGCTGGCCCTTCCCTCCAGGAGCTCAGCCAG	242
Db	120	CACAGCTCCCGATGCTGGGTCTGAGGCTGGCCCTTCCCTCCAGGAGCTCAGCCAG	179
QY	243	TGGGAGTCTGAAGATGGCCAAATACACGCTGGCCACAGAGATGAATATGATCTCTCA	302
Db	180	TGGGAGTCTGAAGATGGCCAAATACACGCTGGCCACAGAGATGAATATGATCTCTCA	239
QY	303	TAGAAGTGAATGGAGAGCGATGAGGACAGCAATGTGACAAGTATGACGCCAGGCAC	362
Db	240	TAGAAGTGAATGGAGAGCGATGAGGACAGCAATGTGACAAGTATGACGCCAGGCAC	299
QY	363	TCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTTGACA	422
Db	300	TCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTTGACA	359
QY	423	ATCTCTGTTGTGTTATCTCGTAAATAATAAAGGACTCAACCGCTGGAAATATCT	482
Db	360	ATCTCTGTTGTGTTATCTCGTAAATAATAAAGGACTCAACCGCTGGAAATATCT	419
QY	483	ATCTCTAAACTTGGCAGTTTCTAACTTGTTGTTCTTGCTTACCTGCCCTTCTGGCTC	542
Db	420	ATCTCTAAACTTGGCAGTTTCTAACTTGTTGTTCTTGCTTACCTGCCCTTCTGGCTC	479
QY	543	ATGCTGGGGCGATCCATGTGTAAATTTCTCAATGGACTGTACTTGTGGGCTGTACA	602
Db	480	ATGCTGGGGCGATCCATGTGTAAATTTCTCAATGGACTGTACTTGTGGGCTGTACA	539
QY	603	GTGAGACATTTTCAATTCCTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGG	662
Db	540	GTGAGACATTTTCAATTCCTCTGACTGTGCAAGGTACTAGTGTGTTTGTGCAAGG	599
QY	663	GCACATTTTCTCAGCCAGGAGGGTCCCTGTGGCATATTACAGTGTCTGGCAT	722
Db	600	GCACATTTTCTCAGCCAGGAGGGTCCCTGTGGCATATTACAGTGTCTGGCAT	659
QY	723	GGTAAACAGCCA-TTCTGGCCACTTTG-CCTGAATACGTGGTTTATAAACCTCAGATGA	780
Db	660	GGTAAACAGCCATTTCTGGCCACTTTGCCCTGAATACGTGGTTTATAAACCTCAGATGA	719
QY	781	AGACCAAAATACAAGTGTGCAATTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATT	840
Db	720	AGACCAAAATACAAGTGTGCAATTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATT	779
QY	841	CTGGAAGCATTTTCTGACTTTTAAATATGAACATTTCCGTTCTGTCTCTCC	891
Db	780	CTGGAAGCATTTTCTGACTTTTAAATATGAACATTTCCGTTCTGTCTCTCC	830

RESULT 2	
BI819787	
LOCUS	BI819787
DEFINITION	603041489F1 NTH_MGC_115 Homo sapiens cDNA clone IMAGE:5182006 5', mRNA sequence.
ACCESSION	BI819787
VERSION	BI819787.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	1 (bases 1 to 880)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM11454 row: b column: 23
High quality sequence stop: 809.

FEATURES
source
1..880
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5182006"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 44.9%; Score 763; DB 4; Length 880;
Best Local Similarity 95.5%; Pred. No. 1.4e-211;
Matches 841; Conservative 0; Mismatches 30; Indels 10; Gaps 5;

QY	19	CTGAGGCTCGGGAGCTTTTGGTACTTATTTACGTTGGTCTCCCTGAGCTCGGTGAGT	78
Db	1	CTGAGGCTCGGGAGCTTTTGGTACTTATTTACGTTGGTCTCCCTGAGCTCGGTGAGT	60
QY	79	GGGGCGGTAGAGCCACAGGGGAATCAACAGTGGTTTCTGTGCCCTCAGGGTCAGGA	138
Db	61	GGGGCGGTAGAGCCACAGGGGAATCAACAGTGGTTTCTGTGCCCTCAGGGTCAGGA	120
QY	139	GCAGTCTCATCAAAAGAGGGGCATCCACTGTCCGGGGCCATTCCACAGTCCCGGATGC	198
Db	121	GCAGTCTCATCAAAAGAGGGGCATCCACTGTCCGGGGCCATTCCACAGTCCCGGATGC	180
QY	199	TGGGTCTGGAGCTGGGCCCTTCCCTCAGGAGCTCAGCCAGTGGGAGTCTGAAGAT	258
Db	181	TGGGTCTGGAGCTGGGCCCTTCCCTCAGGAGCTCAGCCAGTGGGAGTCTGAAGAT	240
QY	259	GGCCAAATTACAGCTGGCCACAGAGATGAATATCATGTCTCTATAGAGGTGAATGGA	318
Db	241	GGCCAAATTACAGCTGGCCACAGAGATGAATATCATGTCTCTATAGAGGTGAATGGA	300
QY	319	GAGCGATGAGGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCAGCTGGT	378
Db	301	GAGCGATGAGGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCAGCTGGT	360
QY	379	GCCATCACTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGNCAATCTCTGGTGTGCT	438
Db	361	GCCATCACTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGNCAATCTCTGGTGTGCT	420
QY	439	TATCTGTGTAATAATAAAGGACTCAAAAGCGGTGAAATAATCTATCTCTAAACTTGGC	498
Db	421	TATCTGTGTAATAATAAAGGACTCAAAAGCGGTGAAATAATCTATCTCTAAACTTGGC	480
QY	499	AGTTTCTAACTTGTGTTTCTTGTCTTACCTGCCCTTCTGGGCTCATGTGGGGGATCC	558
Db	481	AGTTTCTAACTTGTGTTTCTTGTCTTACCTGCCCTTCTGGGCTCATGTGGGGGATCC	540


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ACCESSION CD370587
VERSION CD370587.1 GI:31154677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
    source
        Location/Qualifiers
            1..729
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="UI-H-Ftl1-BKC-j-11-0-UI"
                /tissue_type="Alveolar Macrophage"
                /dev_stage="Adult"
                /lab_host="PH108 (Life Technologies)"
                /clone_lib="NCI_CGAP_Ftl1"
                /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
                modified polylinker; Site 1: EcoR I; Site 2: Not I;
                NCI_CGAP Ftl1 is a normalized cDNA library constructed from
                a pool of 81 RNA samples from Alveolar Macrophages
                challenged with different treatments. The mRNA samples
                were a mixture of these conditions (times refer to
                incubations following isolation by bronchoalveolar lavage)
                (some normal donor macrophages were cultured in some of
                the conditions, other donor macrophages in different
                conditions). The mRNA samples were pooled for library
                construction. Control 0 hours; control 3 hours; control 24
                hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector
                (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500,
                3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                hours; wt adenovirus + LPS 24 hours. The library was
                normalized according to Bonaldo, Lennon and Soares, Genome
                Research, 6:791-806, 1996. First strand cDNA synthesis was
                primed with an oligo-dT primer containing a Not I site.
                Double stranded cDNA was ligated to an EcoR I adaptor,
                digested with Not I, and cloned directionally into
                pT73-Pac vector. The oligonucleotide used to prime the
                synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (dT)18 tail. The sequence tag for this library is
                GGCCATGCGG. The tissue was provided by Dr. Gary W.
                Hunninghake of the University of Iowa.
                TAG LIB=UI-H-Ftl1
                TAG_SEQ=GGCCATGCGG"

ORIGIN
Query Match 40.6%; Score 689; DB 6; Length 729;
Best Local Similarity 99.7%; Pred. No. 6.3e-190;
Matches 711; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 627 TGACTGTGCAAGGTACCTAGTGTGTTTTCACAGGGCAACTTTTCTCAGCCAGGAGA 686

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Db 729 TGACTGTGCAAGGTACCTAGTG-TTTTGCACAGGGCAAC-TTTTCTCAGCCAGGAGA 672
QY 687 GGGTGCCCTGTGGCATTATTAAAGTGTCTGGCATGGGTAAACGCCATTCTGGGCACATT 746
Db 671 GGGTGCCCTGTGGCATTATTAAAGTGTCTGGCATGGGTAAACGCCATTCTGGGCACATT 612
QY 747 TGCCTGAATACGTGGTTTATTAACCTCAGATGGAGACACAGAAATACAAAGTGTGCATTTA 806
Db 611 TGCCTGAATACGTGGTTTATTAACCTCAGATGGAGACACAGAAATACAAAGTGTGCATTTA 552
QY 807 GCAGAACTCCCTTCTCGCCAGCTGATGAGACATTCTCGAAGCATTTTCTGACTTTAAAAAA 866
Db 551 GCAGAACTCCCTTCTCGCCAGCTGATGAGACATTCTCGAAGCATTTTCTGACTTTAAAAA 492
QY 867 TGAACATTTCGGTTCTTCTCTCCCTTATTTATTTTACATTTCTCTATGFGCAAAATGA 926
Db 491 TGAACATTTCGGTTCTTCTCTCCCTTATTTATTTTACATTTCTCTATGFGCAAAATGA 432
QY 927 GAAAAACACTAAGGTTCAAGGAGCAGAGGTATAGCTTTTCAAGCTTGTTTTGGCCATAA 986
Db 431 GAAAAACACTAAGGTTCAAGGAGCAGAGGTATAGCTTTTCAAGCTTGTTTTGGCCATAA 372
QY 987 TGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTGTCCACTTTTCA 1046
Db 371 TGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGCAATTTTCTGTCCACTTTTCA 312
QY 1047 AAGAACACTTCTCCCTGAGTGAAGAGCAGCTACAATCTGAGCAAAAAGTGTTCACA 1106
Db 311 AAGAACACTTCTCCCTGAGTGAAGAGCAGCTACAATCTGAGCAAAAAGTGTTCACA 252
QY 1107 TCACATAACTCATGCGCACCCCACTGCTGCATCAACCTCTCCTGTATGCGTTTCTTG 1166
Db 251 TCACATAACTCATGCGCACCCCACTGCTGCATCAACCTCTCCTGTATGCGTTTCTTG 192
QY 1167 ATGGGACATTTAGCAAAATACCTCTGCCCTGTGTTCCATCTGGTAGTAACACCCCACTTC 1226
Db 191 ATGGGACATTTAGCAAAATACCTCTGCCCTGTGTTCCATCTGGTAGTAACACCCCACTTC 132
QY 1227 AACCAGGGGCGAGTCTGCAAAAGCAGCATCGAGGGAAGAACCTGACCATTTCCACCGAAG 1286
Db 131 AACCAGGGGCGAGTCTGCAAAAGCAGCATCGAGGGAAGAACCTGACCATTTCCACCGAAG 72
QY 1287 TGTAACCTAGCATCCACCAATGCAAGAGATTAACATGATTTTCATCTTT 1339
Db 71 TGTAACCTAGCATCCACCAATGCAAGAGATTAACATGATTTTCATCTTT 19

RESULT 5
CFI47784
LOCUS AGENCOURT_14740191 NIH_MGC_145 Homo sapiens cDNA clone
DEFINITION IMAGE:6971947 5', mRNA sequence.
ACCESSION CFI47784
VERSION CFI47784.1 GI:33244052
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 716)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

```


Db 301 TATGAGCCAGGACCTCTCAGCCAGCTGGTGCATCACTCTGCTCTGCTG-TTGTG 359
QY 407 ATCGGTGCTCTGACCAATCTCTGCTGTGTCTTATCTCTGTTAAATATAAAGGACTCAAA 466
Db 360 ATCGGTGCTCTGACCAATCTCTGCTGTGTCTTATCTCTGTTAAATATAAAGGACTCAAA 419
QY 467 CGGTGGAAATATCTCTTAACTTTGAGGAGTTTCTAACTGTGTTCTTGTCTTACC 526
Db 420 CGGTGGAAATATCTCTTAACTTTGAGGAGTTTCTAACTGTGTTCTTGTCTTACC 479
QY 527 CTGCCCCCTCTGCGCTCATCTCTGGGGCGATCCCATGTGTAAATTTCTCAATGCACTGTAC 586
Db 480 CTGCCCCCTCTGCGCTCATCTCTGGGGCGATCCCATGTGTCAATTTCTCA-TGACCTGTAC 538
QY 587 TTCTGTGGGCTGTACAGTGAACATTTTCAATTTGCTTCTGACTGTGTGCAAAAGGTACCTTA 646
Db 539 TTCTGTGGGCTGTACAGTGAACATTTTCAATTTGCTTCTGACTGTGTGCAAAAGGTACCTTA 598
QY 647 GTGTTTTCACAGGCACTTTTCTCAGCCAGGAGGAGGTCCTGTGGCATCATTT 706
Db 599 GTG-TTTTGCACAAGGGCACTTTTCTCAGCCAGGAGGAGGTCCTGTGGCATCATTT 657
QY 707 ACAAGTGTCTGGCATGGTAACAGCCATTCTGGCCACTTTTGCCTGAATACGCTGGTTTAT 766
Db 658 ACAAGTGTCTGGCATGGTAACAGCCAGTCTGGCCACTTTGACATGATACGCTGGTTTAT 717
QY 767 AAACCTCAGATGGAAGACAGCAAAATACAAAGTGT 799
Db 718 AAACCTCAGATGGAAGACAGCAATCCAGTGT 750

RESULT 7
BG386374 1035 bp mRNA linear EST 12-MAR-2001
LOCUS 60245580F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4584043 5',
DEFINITION mRNA sequence.

ACCESSION BG386374

VERSION BG386374.1 GI:13279820

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL 1 (bases 1 to 1035)

COMMENT NIH-MGC http://mgi.nci.nih.gov/.

CONTACT National Institutes of Health, Mammalian Gene Collection (MGC)

UNPUBLISHED (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cga@bbs-r@mail.nih.gov

TISSUE Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: NIH Intramural Sequencing Center

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

http://image.llnl.gov

Plate: LLM1308 row: o column: 20

High quality sequence stop: 626.

Location/Qualifiers

1..1035

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4584043"

/tissue_type="adenocarcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 15"

/note="Organ: colon; Vector: pOTB7; Site: 1: XhoI; Site 2:

ECORI; CDNA made by oligo-dT priming. Directionally

cloned into EORI/XhoI sites using the following 5'

adapter: GGACACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies) "

ORIGIN

Query Match 38.1%; Score 646.4; DB 4; Length 1035;

Best Local Similarity 95.2%; Pred. No. 2.e-177;

Matches 720; Conservative 0; Mismatches 31; Indels 5; Gaps 5;

QY 19 CTGAGGCGCTGGGGAGCTTTTGAGTACTTTATTTTCAGTTGCTCCCTGAGCTCGGTGAGT 78

Db 2 CTGAGGCGCTGGGGAGCTTTTGAGTACTTTATTTTCAGTTGCTCCCTGAGCTCGGTGAGT 61

QY 79 GGGGGGGGTAGAGCCACAGGGGATCAACAGTGTCTCGTGGCCCTCAGGGTCAGGA 138

Db 62 GGGGGGGGTAGAGCCACCA-GGGAAATCAACAGTGTCTCGTGGCCCTCAGGGTCAGGA 120

QY 139 GCAGTCTCATCAAAAGGAGGGCATCCACTGTCCGGGGCCATTCCACAGCTCCCGGATGC 198

Db 121 GCAGTCTCATCAAAAGGAGGGCATCCACTGTCCGGGGCCATTCCACAGCTCCCGGATGC 180

QY 199 TGGGTCTGAGGCTCGGCCCTTCCCTTCAGGAGCTCAGCCAGTGGGAGTCTGAA-GA 257

Db 181 TGGGTCTGAGGCTCGGCCCTTCCCTTCAGGAGCTCAGCCAGTGGGAGTCTGAA-CGA 240

QY 258 TGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCTCATAGAAGTGAACCTGG 317

Db 241 TGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCTCATAGAAGTGAACCTGG 300

QY 318 AGAGCGATGAGGCGAGCAATGTGACAAAGTATGAGCCCGAGGCACTCTCAGCCAGCTGG 377

Db 301 AGAGCGATGAGGCGAGCAATGTGACAAAGTATGAGCCCGAGGCACTCTCAGCCAGCTGG 360

QY 378 TGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTTCTCTGGACAATCTCTGTTGTGTC 437

Db 361 TGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTTCTCTGGACAATCTCTGTTGTGTC 420

QY 438 TTATCTCTGTAATAATATAAAGGACTCAAAACGGTGGAAATATCTCTTCTAACTTGG 497

Db 421 TTATCTCTGTAATAATATAAAGGACTCAAAACGGTGGAAATATCTCTTCTAACTTGG 480

QY 498 CAGTTTCTTAACCTGTGTTTCTTGTCTTACCTTCCCTTCTGGGCTCATGCTGGGGCGATC 557

Db 481 CAGTTTCTTAACCTGTGTTTCTTGTCTTACCTTCCCTTCTGGGCTCATGCTGGGGCGATC 540

QY 558 CCAATGTGTAATAATCTCTATTGACATGTTGCTGGGCTGTACAGTGAGACATTTTCA 617

Db 541 CCAATGTGTAATAATCTCTATTGACATGTTGCTGGGCTGTACAGTGAGACATTTTCA 600

QY 618 ATTGCTTCTGACCTGTGCAAAAGGTACCT-AGTGTGTTTTCACAGGGCACTTTTCTCA 676

Db 601 ATTGCTTCTGACCTGTGCAAAAGGTACCT-AGTGTGTTTTCACAGGGCACTTTTCTCA 660

QY 677 GCCAGGAGGAGGTCCTTGTGGCATCATTTACA-AGTGTCTTGGCATGGGTAAACGCCAT 735

Db 661 GCCAGGAGGAGGTCCTTGTGGCATCATTTACAAGTGTCTTGGCATGGGTAAACGCCAT 720

QY 736 TC-TGGCCACTTTGCTGCAATACGTGTTTATAAAC 770

Db 721 TCTTGGCCACTTTGCTGCAATTCGGTGGTTATAAGC 756

RESULT 8

CD520843

LOCUS

DEFINITION

AGNCOURT 14369985 NIH_MGC_191 Homo sapiens cDNA clone

IMAGE:30409698 5', mRNA sequence.

ACCESSION

CD520843

VERSION

CD520843.1 GI:31452561

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CD520843 720 bp mRNA linear EST 06-JUN-2003

AGNCOURT 14369985 NIH_MGC_191 Homo sapiens cDNA clone

IMAGE:30409698 5', mRNA sequence.

ACCESSION

CD520843

VERSION

CD520843.1 GI:31452561

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match 35.2%; Score 597.6; DB 7; Length 773;
Best Local Similarity 98.6%; Pred. No. 4e-163; 8; Indels 1; Gaps 1;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 TTTTCTCAGCAGGAGGAGGCTGCTGGCATCATTAACAAGTGTCTGGCATGGGTAAC 729
DB |||||
QY 638 TTTTTCAGCAGAGGAGGCTGCTGGCATCATTAACAAGTGTCTGGCATGGGTAAC 579
DB |||||

QY 730 AGCCATTCTGGCAGCTTTCCTGGAATACCTGTTTATAAACTCAGATGGAAGACAGAA 789
DB |||||

QY 578 AGCCATTCTGGCAGCTTTCCTGGAATACCTGTTTATAAACTCAGATGGAAGACAGAA 519
DB |||||

QY 790 ATACAAGTGTGATTTAGCAGAACTCCCTTCCTGCGAGCTGATGACATCTCGAAGCA 849
DB |||||

QY 518 ATACAAGTGTGATTTAGCAGAACTCCCTTCCTGCGAGCTGATGACATCTCGAAGCA 459
DB |||||

QY 850 TTTTCTGACTTTAAAAATGAAACATTTCCGTTCTTGTCTCCCTTATTTATTTTACATT 909
DB |||||

QY 458 TTTTCTGACTTTAAAAATGAAACATTTCCGTTCTTGTCTCCCTTATTTATTTTACATT 399
DB |||||

QY 910 TCTCTATGTGCAAAATGAGAAAAACACTAAGTTTCAGGGAGCAGAGGTATAGCCTTTTCAA 969
DB |||||

QY 398 TCTCTATGTGCAAAATGAGAAAAACACTAAGTTTCAGGGAGCAGAGGTATAGCCTTTTCAA 339
DB |||||

QY 970 GCTTGTGTTTGGCATAATGGTAGTCTTCCCTCTGTGTTGGGCGCCCTACAATATTGCATT 1029
DB |||||

QY 338 GCTTGTGTTTGGCATAATGGTAGTCTTCCCTCTGTGTTGGGCGCCCTACAATATTGCATT 279
DB |||||

QY 1030 TTTTCTGTGCTCACTTTCAAGAGAACATTTCTCCCTGTAGTCTGCAAGAGCAGCTACAATCT 1089
DB |||||

QY 278 TTTTCTGTGCTCACTTTCAAGAGAACATTTCTCCCTGTAGTCTGCAAGAGCAGCTACAATCT 219
DB |||||

QY 1090 GGACAAAAGTGTTCATCACTAAACTCATGCAAGCACCACCTCTGTGTCATCAACCTCT 1149
DB |||||

QY 218 GGACAAAAGTGTTCATCACTAAACTCATGCAAGCACCACCTCTGTGTCATCAACCTCT 159
DB |||||

QY 1150 CTTGTATGCTTCTGTGAGGACATTTAGCAAACTCTGCGCTGTTTCCATCTGG 1209
DB |||||

QY 158 CTTGTATGCTTCTGTGAGGACATTTAGCAAACTCTGCGCTGTTTCCATCTGG 99
DB |||||

QY 1210 TAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGAAGAAC 1269
DB |||||

QY 98 TAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGCACATCGAGGGAAGAAC 39
DB |||||

QY 1270 TGACCATTCACCGAAGTGTA 1290
DB |||||

QY 38 TGACCA-TCCACCGAAGTGTA 19
DB |||||

RESULT 10
BP300486 581 bp mRNA linear EST 17-SEP-2004
LOCUS
DEFINITION BP300486 Sugano cDNA library, macrophage Homo sapiens cDNA clone
MPE01252, mRNA sequence.
ACCESSION BP300486
VERSION BP300486.1 GI:52229446
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
Location/Qualifiers

source 1. 581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MP01252"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

ORIGIN

Query Match 34.2%; Score 581; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.6e-158;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACGCTTCAGAGATCCTCTGAGGCGCTGGGGAGCTTTTGAGTACTTTATTTTCAGTTGG 60
DB 1 AGACGCTTCAGAGATCCTCTGAGGCGCTGGGGAGCTTTTGAGTACTTTATTTTCAGTTGG 60

QY 61 TCCCTGAGCTCGGTGAGTGGGCGGTAGAGCCACAGGGGAATCAACAGTGTGTTCTCG 120
DB |||||

QY 61 TCCCTGAGCTCGGTGAGTGGGCGGTAGAGCCACAGGGGAATCAACAGTGTGTTCTCG 120
DB |||||

QY 121 TGCCCTTCAGGGTCAGGAGCAGTCTGATCAAAAAGAGGGCATCCACTGTCCGGGGCCATT 180
DB |||||

QY 121 TGCCCTTCAGGGTCAGGAGCAGTCTGATCAAAAAGAGGGCATCCACTGTCCGGGGCCATT 180
DB |||||

QY 181 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTGCAGGAGCTCAGCCC 240
DB |||||

QY 181 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTGCAGGAGCTCAGCCC 240
DB |||||

QY 241 AGTGGGCACTCTGAAGATGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCCT 300
DB |||||

QY 241 AGTGGGCACTCTGAAGATGGCCAAATTACACGCTGGCACAGAGGATGAATATGATGTCCT 300
DB |||||

QY 301 CATGAAGGTGAATCTGGAGAGCATGAGGAGAGCAATGTGACAAAGTATGAGCCGAGCC 360
DB |||||

QY 301 CATGAAGGTGAATCTGGAGAGCATGAGGAGAGCAATGTGACAAAGTATGAGCCGAGCC 360
DB |||||

QY 361 ACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTCTCTGGA 420
DB |||||

QY 361 ACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTCTCTGGA 420
DB |||||

QY 421 CAATCTCTGTTGTGCTTATCTCGTAAAAATATAAGGACTCAAAACGCGTGAATAAT 480
DB |||||

QY 421 CAATCTCTGTTGTGCTTATCTCGTAAAAATATAAGGACTCAAAACGCGTGAATAAT 480
DB |||||

QY 481 CTATCTCTAAACTTTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCTGCTTCTGGGC 540
DB |||||

QY 481 CTATCTCTAAACTTTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCTGCTTCTGGGC 540
DB |||||

QY 541 TCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGAC 581
DB |||||

QY 541 TCATGCTGGGGCGATCCCATGTGTGTAAATTTCTCATTTGGAC 581
DB |||||

RESULT 11
BP295805 576 bp mRNA linear EST 17-SEP-2004
LOCUS
DEFINITION BP295805 Sugano cDNA library, macrophage Homo sapiens cDNA clone
MP09014, mRNA sequence.
ACCESSION BP295805
VERSION BP295805.1 GI:52224765
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 576)
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezukui@ims.u-tokyo.ac.jp.

Location/Qualifiers
1..576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MPB09014"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

Query Match 33.8%; Score 573.4; DB 5; Length 576;
Best Local Similarity 99.7%; Pred. No. 4.4e-156;
Matches 574; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGGTC 62
DB 1 ACCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGGTC 60
QY 63 CCTGAGCTCGTCACTGGGGCGGTAGAGCCAGCGGGAATCAACAGTGGTTCTCGTG 122
DB 61 CCTGAGCTCGTCACTGGGGCGGTAGAGCCAGCGGGAATCAACAGTGGTTCTCGTG 120
QY 123 CCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGCGCATCCACTGTCCGGGGCCATTCC 182
DB 121 CCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGCGCATCCACTGTCCGGGGCCATTCC 180
QY 183 CACAGTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTTCAGGAGCTCAGCCCCAG 242
DB 181 CACAGTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTTCAGGAGCTCAGCCCCAG 240
QY 243 TGGGCACTCTGAAGTGGCCAAATACACGCTGCGAGGATGATATGATGTCCTCA 302
DB 241 TGGGCACTCTGAAGTGGCCAAATACACGCTGCGAGGATGATATGATGTCCTCA 300
QY 303 TAGAAGGTGAATGGAGAGCGATGAGCGAGCAATGTGACAAAGTATGAGCGCCAGGCAC 362
DB 301 TAGAAGGTGAATGGAGAGCGATGAGCGAGCAATGTGACAAAGTATGAGCGCCAGGCAC 360
QY 363 TCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGACA 422
DB 361 TCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGACA 420
QY 423 ATCTCTGCTGTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAATATCT 482
DB 421 ATCTCTGCTGTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAATATCT 480
QY 483 ATCTCTAAACTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCTCTGGGCTC 542
DB 481 ATCTCTAAACTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCTCTGGGCTC 540
QY 543 ATGCTGGGGCGATCCCATGTGTPAAAATTCCTATTG 578
DB 541 ATGCTGGGGCGATCCCATGTGTPAAAATTCCTATTG 576

RESULT 12
BP300273
LOCUS
DEFINITION
BP300273 Sugano cDNA library, macrophage Homo sapiens cDNA clone
MPE00730, mRNA sequence.
ACCESSION
BP300273
VERSION
BP300273.1 GI:52229233
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 581)
AUTHORS
Suzuki.Y., Yamashita.R., Shiota,M., Sakakibara.Y., Chiba.J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezukui@ims.u-tokyo.ac.jp.

Location/Qualifiers
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MPE00730"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"

Query Match 32.6%; Score 553.4; DB 5; Length 581;
Best Local Similarity 99.8%; Pred. No. 3.2e-150;
Matches 554; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGACGCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGG 60
DB 27 AGACGCTTCAGAGATCCTCTGGAGGCTGGGGAGCTTTTGAGTACTTTTATTTTCAGTTGG 86
QY 61 TCCTTGAGCTCGGTGAGTGGGGCGGTAGAGCCAGCGGGAATCAACAGTGGTTCTCG 120
DB 87 TCCTTGAGCTCGGTGAGTGGGGCGGTAGAGCCAGCGGGAATCAACAGTGGTTCTCG 146
QY 121 TGCCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGCGCATCCACTGTCCGGGGCCATT 180
DB 147 TGCCCTCAGGCTCAGGAGCAGTCTGATCAAAAGAGGCGCATCCACTGTCCGGGGCCATT 206
QY 181 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTTCAGGAGCTCAGCCCC 240
DB 207 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTTCAGGAGCTCAGCCCC 266
QY 241 AGTGGGCACTCTGAAGTGGCCAAATTACACGCTGGCCAGGAGGATGATATGATGTCCT 300
DB 267 AGTGGGCACTCTGAAGTGGCCAAATTACACGCTGGCCAGGAGGATGATATGATGTCCT 326
QY 301 CATAGAAGTGAATCTGGAGAGCGATGAGCGAGCAATGTGACAAAGTATGACGCCAGGC 360
DB 327 CATAGAAGTGAATCTGGAGAGCGATGAGCGAGCAATGTGACAAAGTATGACGCCAGGC 386
QY 361 ACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGA 420
DB 387 ACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGCTCTGGA 446
QY 421 CAATCTCTGGTTGTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAATAT 480
DB 447 CAATCTCTGGTTGTGCTTATCTCTGTTAAATATATAAGGACTCAACCGGTGGAAATAT 506
QY 481 CTATCTTTAAACTTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCTTCTGGGC 540
DB 507 CTATCTTTAAACTTGGCAGTTTCTAACTGTGTTTCTTGTCTTACCTGCCCTTCTGGGC 566
QY 541 TCATGCTGGGGCGA 555
DB 567 TCATGCTGGGGCGA 581

RESULT 13
AW300833/c
LOCUS
DEFINITION
AW300833
similar to TR:000421 000421 CCR6. [1] ; mRNA sequence.
ACCESSION
AW300833
VERSION
AW300833.1 GI:6710510
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Meskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
Location/Qualifiers
1. 573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2665980"
/issue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col9"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot 50. Average insert size 1.32Kb.
Normalized version of NCI CGAP_Col8. Library constructed
by Life Technologies."

ORIGIN
Query Match 32.1%; Score 545.8; DB 2; Length 573;
Best Local Similarity 98.4%; Pred. No. 5.4e-148;
Matches 561; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 1130 CACTGCTGCATCAACCTCT-CCTGTATGCGTTCTTGTATGGACATTTAGCAATACCT 1188
DB 573 CACTGCTGCATCAACCTCTCCTGTATGCGTTCTTGTATGGACATTTAGCAATACCT 514
QY 1189 CTGCCGCTGTTCCTAGTACCTGCTAGTAAACCCCACTTCAACCGGGGCGAGTCTGCACA 1248
DB 513 CTGCCGCTGTTCCTAGTACCTGCTAGTAAACCCCACTTCAACCGGGGCGAGTCTGCACA 454
QY 1249 AGGCACATCGAGGAGAACCTGACCATTCACCGAGTGTAACTAGCATCCACCAAT 1308
DB 453 AGGCACATCGAGGAGAACCTGACCATTCACCGAGTGTAACTAGCATCCACCAAT 394
QY 1309 GCAAGAAGATAAATCAATGATTTTCATCTTCTGCAATTTTCATGTAATTTCTACAC 1368
DB 393 GCNAGAAGATAAATCAATGATTTTCATCTTCTGCAATTTTCATGTAATTTCTACAC 334
QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAACTTTGCTAAGC 1428
DB 333 ATTTGTATACAAATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAACTTTGCTAAGC 274
QY 1429 ACTGAATTTGCTCAGGACCGTGCAGGCTCTTTTACAACTGAGCTCTTCGCTCCT 1488
DB 273 ACTGAATTTGCTCAGGACCGTGCAGGCTCTTTTACAACTGAGCTCTTCGCTCCT 214
QY 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGG 1548
DB 213 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGG 154
QY 1549 CGGAAATTTGCTTAAGATCACTTAATAGGAAGTGGCAGAACTGATTTCCAGCCCTGTT 1608
DB 153 CGGAAATTTGCTTAAGATCACTTAATAGGAAGTGGCAGAACTGATTTCCAGCCCTGTT 94
QY 1609 AGCATTTGCTCAGAGCTAGCTTGGTCCAGACATCAAACTCCAAACCTTGGGGACAA 1668

Db 93 AGCATTTGCTCAGACCTTACGCTTGTTCAGACATCAAACTCCAAACCTTGGGGACAA 34
QY 1669 CGACATGAATAAATGATTTTAAACATC 1698
Db 33 CGACATGAATAAATGATTTTAAACATC 4
RESULT 14
LOCUS AI343408 547 bp mRNA linear EST 08-APR-1999
DEFINITION tb96a06.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2062162 3'
similar to TR:000421 000421 CCR6. ; mRNA sequence.
ACCESSION AI343408
VERSION AI343408.1 GI:4080614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 630 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
1. 547
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2062162"
/issue_type="colon tumor, RER+"
/lab_host="DH10B"
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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
modified Polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 30.6%; Score 520.4; DB 1; Length 547;
Best Local Similarity 99.3%; Pred. No. 1.5e-140;
Matches 543; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1154 TATGCGTTTCTTGTATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGGTAGT 1213
DB 547 TATGCGTTTCTTGTATGGACATTTAGCAAAATACCTCTGCGCTGTTTCCATCTCGGTAGT 488
QY 1214 RACA-CCCCACTCAACCCAGGGGCGAGTCTGCACAGGCACATCGAGGAGAAAC-CCGTG 1271
DB 487 AACACCCCCACTTCAACNCAGGGGCGAGTCTGCACAGGCACATCGAGGAGAAACCCCTG 428
QY 1272 ACCATTCCACCCGAGGTGTAACCTAGCATCCACCAATGCAAGAATAAATGATTT 1331
DB 427 ACCATTCCACCCGAGGTGTAACCTAGCATCCACCAATGCAAGAATAAATGATTT 368

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QY 1332 TCATCTTTCTGCATATTTCATGTAATTTTCTACACATTTGTATACAAATCGGATACA 1391
    |||||
Db 367 TCATCTTTCTGCATATTTCATGTAATTTTCTACACATTTGTATACAAATCGGATACA 308

QY 1392 GGAAGAAAGGAGAGGTAGCTAAACATTTGCTAAGCACTGAATTTGTCTCAGGACCGT 1451
    |||||
Db 307 GGAAGAAAGGAGAGGTAGCTAAACATTTGCTAAGCACTGAATTTGTCTCAGGACCGT 248

QY 1452 GCAAGGCTCTTTACAAACGTGAGCTCTTCGCGCTCCTACCACTTGTCATAGTGTGGATA 1511
    |||||
Db 247 GCAAGGCTCTTTACAAACGTGAGCTCTTCGCGCTCCTACCACTTGTCATAGTGTGGATA 188

QY 1512 GGAAGTCTCTATTTCTCTGAGAAGAAACTAAGGCGCGGAAATTTGTCTAAGATCACAT 1571
    |||||
Db 187 GGAAGTCTCTATTTCTCTGAGAAGAAACTAAGGCGCGGAAATTTGTCTAAGATCACAT 128

QY 1572 AACTAGAAAGTGGAGAACTGATTTCTCCAGCCCTGTGTAGCATTTGTCTCAGAGCTACGCT 1631
    |||||
Db 127 AACTAGAAAGTGGAGAACTGATTTCTCCAGCCCTGTGTAGCATTTGTCTCAGAGCTACGCT 68

QY 1632 TGGTCCAGAACATCAAACTCCAAACCTCGGGGACAAACGACATGAATTAATGATTTTA 1691
    |||||
Db 67 TGGTCCAGAACATCAAACTCCAAACCTCGGGGACAAACGACATGAATTAATGATTTTA 8

QY 1692 AAACATC 1698
    |||||
Db 7 AAACATC 1
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RESULT 15
BX480211
LOCUS
DEFINITION
  DXFzp686i16218_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
  DXFzp686i16218 5', mRNA sequence.
ACCESSION
  BX480211
VERSION
  EST.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 517)
  Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
  Fobo,G., Han,W. and Wiemann,S.
  EST (Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., et al.)
  Unpublished (2003)
  Contact: MIPS
  MIPS
  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
  This is the 5' sequence of the clone insert
  Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
  Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
  sequenced by GBF (National Research Centre for Biotechnology Ltd.,
  Braunschweig/Germany) within the cDNA sequencing consortium of the
  German Genome Project.
  No 5' sequence available.
  This clone (DXFzp686i16218) is available at the RZPD in Berlin.
  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
  Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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FEATURES
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      /db_xref="taxon:9606"
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      /dev_stage="adult"
      /lab_host="DH10B"
      /clone_lib="686 (synonym: hlcc3)"
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      cDNA-collection"
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ORIGIN

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Best Local Similarity 98.8%; Pred. No. 2e-128;
Matches 482; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGACGGTTCAGAGATCCTCTGGAGGCTCTGGGGAGCTTTTGTAGTACTTTATTTTCAGTTGG 60
    |||||
Db 30 AGACGGTTCAGAGATCCTCTGGAGGCTCTGGGGAGCTTTTGTAGTACTTTATTTTCAGTTGG 89

QY 61 TCCTCTCAGCTCCGGTGTAGTGGGGGGGTAGAGCCACCAGGGGAATCAACAGTGTGTTCTCG 120
    |||||
Db 90 TCGGGAGGCTCGGGTGTAGTGGGGGGGTAGAGCCACCAGGGGAATCAACAGTGTGTTCTCG 149

QY 121 TGCCCCCTCAGGGTTCAGGAGCAGTCTGATCAAAAGGAGGGGATCCACCTGTCCGGGGCCATT 180
    |||||
Db 150 TGCCCCCTCAGGGTTCAGGAGCAGTCTGATCAAAAGGAGGGGATCCACCTGTCCGGGGCCATT 209

QY 181 CCACAGCTCCCGGATGCTGGGCTGTGGAGGCTGCGCCCTTCCCTCGAGAGCTCAGCCC 240
    |||||
Db 210 CCACAGCTCCCGGATGCTGGGCTGTGGAGGCTGCGCCCTTCCCTCGAGAGCTCAGCCC 269

QY 241 AGTGGGCACTCTGAAGATGCGCCAAATTACACGCTGGCCACCAGAGGATGATATGATGTCCT 300
    |||||
Db 270 AGTGGGCACTCTGAAGATGCGCCAAATTACACGCTGGCCACCAGAGGATGATATGATGTCCT 329

QY 301 CATAGAAGTGAATCTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCAGGC 360
    |||||
Db 330 CATAGAAGTGAATCTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCAGGC 389

QY 361 ACTCTCAGCCCCAGCTGGTCCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCCTGGA 420
    |||||
Db 390 ACTCTCAGCCCCAGCTGGTCCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCCTGGA 449

QY 421 CAATCTCCTGGTGTGCTTATCTCGTAAATATAAAGGACTCAAAACGGGTGGAATATAT 480
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QY 481 CTATCTTC 488
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Db 510 CTATCTTC 517
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Search completed: June 18, 2005, 19:42:01
Job time : 5814 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 15:19:56 ; Search time 306 Seconds
(without alignments)
9079.732 Million cell updates/sec

Title: AF014958
Perfect score: 1698
Sequence: 1 AGACGCTTCAGAGATCCTCT.....TAAATGATTTTAAACATC 1698

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patente NA.*
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6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1448.2	85.3	1547	US-10-039-659A-11	Sequence 11, Appl
2	1268	74.7	1270	US-09-016-434-756	Sequence 756, App
3	981.2	57.8	1050	US-08-681-192-1	Sequence 1, Appli
4	597.8	35.2	620	US-09-023-655-308	Sequence 308, App
5	233	13.7	1059	US-09-517-605-8	Sequence 8, Appli
6	233	13.7	1059	US-08-771-276-19	Sequence 19, Appl
7	230.6	13.6	1059	US-08-724-984A-3	Sequence 3, Appli
8	230.6	13.6	1225	US-09-023-655-967	Sequence 967, App
9	230.6	13.6	1376	US-09-087-232A-12	Sequence 12, Appl
10	230.6	13.6	1376	US-09-016-434-1104	Sequence 1104, Ap
11	230.6	13.6	1376	US-09-796-202-2	Sequence 2, Appli
12	230.6	13.6	1414	US-09-502-783A-1	Sequence 1, Appli
13	230.6	13.6	1414	US-09-339-912A-1	Sequence 1, Appli
14	230.6	13.6	1414	US-09-195-662A-1	Sequence 1, Appli
15	230.6	13.6	1477	US-08-833-752-2	Sequence 2, Appli
16	230.6	13.6	1477	US-09-938-719-2	Sequence 2, Appli
17	230.6	13.6	1477	US-09-939-226B-2	Sequence 2, Appli
18	230.6	13.6	1477	US-08-861-105-13	Sequence 13, Appl
19	230.6	13.6	3383	US-08-575-967A-1	Sequence 1, Appli
20	230.6	13.6	3383	US-09-023-655-951	Sequence 951, App
21	230.6	13.6	3383	US-08-771-276-1	Sequence 1, Appli
22	230.6	13.6	5674	US-09-293-170-3	Sequence 3, Appli
23	230.6	13.6	5674	US-09-826-509-476	Sequence 476, App
24	229	13.5	1059	US-09-087-232A-14	Sequence 14, Appl
25	229	13.5	1071	US-08-466-343D-1	Sequence 1, Appli
26	225.8	13.3	1414	US-08-847-296B-2	Sequence 2, Appli
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28	196.6	11.6	1139	4	US-08-375-199B-3	Sequence 3, Appli
29	196.6	11.6	1193	4	US-08-720-565-3	Sequence 3, Appli
30	196.6	11.6	1201	4	US-09-016-434-1085	Sequence 1085, Ap
31	196.6	11.6	1201	4	US-09-023-655-905	Sequence 905, App
32	196.6	11.6	1717	4	US-09-023-655-959	Sequence 959, App
33	196.6	11.6	1915	3	US-08-575-967A-3	Sequence 3, Appli
34	196.6	11.6	1915	4	US-08-771-276-3	Sequence 1, Appli
35	194	11.4	2440	3	US-08-724-984A-1	Sequence 474, App
36	193.4	11.4	1068	4	US-09-826-509-474	Sequence 1, Appli
37	193.4	11.4	1689	4	US-08-720-565-1	Sequence 15, Appl
38	193.4	11.4	1689	4	US-09-931-381A-15	Sequence 1, Appli
39	193.4	11.4	1689	4	US-08-375-199B-1	Sequence 5, Appli
40	192.6	11.3	1116	4	US-08-720-565-5	Sequence 5, Appli
41	192.6	11.3	1116	4	US-08-375-199B-5	Sequence 1190, Ap
42	189.8	11.2	1495	4	US-09-016-434-1190	Sequence 1021, Ap
43	189.8	11.2	1495	4	US-09-023-655-1021	Sequence 1, Appli
44	189.8	11.2	2156	1	US-08-012-988A-1	Sequence 1247, Ap
45	189.8	11.2	2156	4	US-09-023-655-1247	

ALIGNMENTS

RESULT 1
US-10-039-659A-11
; Sequence 11, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589K1B US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(1116)
; OTHER INFORMATION:
US-10-039-659A-11

Query Match 85.3%; Score 1448.2; DB 4; Length 1547;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1450; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 73 GGCAGTCTCAAGATGCCAAATTACAGCTGGCACACAGAGATGAATATGATGTCCTCATTA 132
QY 305 GAAGGTGAACCTGGAGAGCGATGAGCAGACGAATGTGACAAGTATGACGCCAGGCACTC 364
Db 133 GAAGGTGAACCTGGAGAGCGATGAGCAGACGAATGTGACAAGTATGACGCCAGGCACTC 192
QY 365 TCAGCCAGCTGGTGGCCATCACTCTGCTCTGCTGTTGTTGATCGGTGCTCTGGACAAT 424
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Qy	485	CTTCTAAACTTTGGCAGTTCTTAACCTCTGTGTTTCTTGTCTTACCTCTGCCCTCTTCGGGCTCAT	544
Db	313	CTTCTAAACTTTGGCAGTTCTTAACTTGTGTTTCTTGTCTTACCTCTGCCCTCTTCGGGCTCAT	372
Qy	545	GCTGGGGCGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGT	604
Db	373	GCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGT	432
Qy	605	GAGACATTTTTCAATATGCGCTTCTGACTGTGTGCAAAAGTACCTAGTGTTTTTTGCACAAGGGC	664
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Qy	665	AACTTTTTTCTCAGCAGGAGGAGGTCGCCCTGTGGCATCATTAACAAGTGTCTCGGCATGG	724
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Qy	725	GTAACAGCCATTCTTGGGCACATTTCCCTCGAATACGTGTGTTTATAAACCTCAGATGGAAGAC	784
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Qy	785	CAGAAATACAGTGTGCATTTAGCAGAACTCCCTTCTCTGCGCAGCTGATGAGACATTTCTGG	844
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Qy	965	TTCAAGCTTGTTTTTTGGCCATAATGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATT	1024
Db	793	TTCAAGCTTGTTTTTTGGCCATAATGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATT	852
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Qy	1385	GGATACAGGAAGAAAGGAGAGGTGAGCTAACATTTTGCTTAAGCACTGAATTTGTCCTCAG	1444
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Qy      1685  TATTTTAAACAT 1697
Db      1513  TATTTTAAACAT 1525

RESULT 2
US-09-016-434-756
; Sequence 756, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 756:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MPHGNOT03
; CLONE: 442279
; US-09-016-434-756

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Db 601 CCAGGAGGAGGCTGCTGTGGCATATTACAAGTGTCTGGCATGGGTAAACGCAATTC 660
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QY 1338 TTCTGCATTA 1347
Db 1261 TTCTGCATTA 1270

RESULT 3
US-08-681-192-1
; Sequence 1, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFDS78
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1050 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-681-192-1

Query Match 57.8%; Score 981.2; DB 3; Length 1050;
Best Local Similarity 99.7%; Pred. No. 8.6e-302;
Matches 983; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 306 AAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAGTATGACGCCCGGAGGCACTCT 365
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DB 544 TGTGGTAGGACTAGTCTCTATTTCTCTGAGAGAAATAGGCGCGGAAATTTGTCTAA 603
QY 1564 GATCACTTAACCTAGG 1578
DB 604 GGTACATTAACCTAGG 618
RESULT 5
US-09-517-605-8
; Sequence 8, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-517-605-8
Query Match 13.7%; Score 233; DB 3; Length 1059;
Best Local Similarity 56.8%; Pred. No. 3.2e-63;
Matches 531; Conservative 0; Mismatches 365; Indels 39; Gaps 4;
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DB 678 CGAGAAAGAGGAGCAGAGGCTGTGAGGCTTATCTTCAACCATCATGATTTGTTATTTCT 737
QY 1003 GATGTGGGCGCTCAATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1062
DB 738 CTCTCTGGGCTCCCTACAACATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 797
QY 1063 GAGTGACTGCAAGAGCAGCTTACAATCTGGAACAAAGTGTTCACATCACTAACTCATCGC 1122
DB 798 GAATAATTGCACTAGCTCTAAACAGGTTGGACCAAGCCATGCGAGTGCAGAGACTCTTGG 857
QY 1123 CACCACCACTGCTGATCAACCCCTCTCTCTGATGCTTCTTGTGATGGGACATTTAGCAA 1182
DB 858 GATGAGCAGCTGCTGATCAACCCCATCATCTATGCTTGTGTTGGGAGAGTTTCAGAAA 917
QY 1183 ATACCTCTCGCGCTGTTTCCATCTCGGTAGTAACA 1217
DB 918 CTACCTCTTAGTCTTCTTCCAAAGCATATTGCCA 952
RESULT 6
US-08-771-276-19
; Sequence 19, Application US/08771276
; Patent No. 6797811
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun.
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/771,276
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 679781land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

Db 410 TAAAGCC---AGGACGGTCACTTTGGGGTGTGACAGGTGATCACTTGGGTGGTGG 466
QY 732 CCATCTGGCCACTTTGCCCTGAATACGTGTTTATTAACCTTCAGATGGAAGACCAAGAT 791
Db 467 CTGTGTTGGTCTCTCCAGGATCATCTTTACCAGATCTCAAAAGAAAGGTCTTCATT 526
QY 792 ACAAGTGTGATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTTCTGGAAGCAT 851
Db 527 ACACCT-----GCAGCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGATT 577
QY 852 TTCTGACTTTAAATGAACATTTGCTTCTTGTCTTCCCTCCCTATTATTTTACATTTC 911
Db 578 TCAGACATTAAGATAGTATCATCTGGGGTGTGCTTCCCTGCTGCTTGTGATGTCATCT 637
QY 912 TCTATGTGCAATGAGAAAAACACTA-----AGTTTCAGGGACAGGTATAGCC 962
Db 638 GCTACTCGGAATCTTAAACCTCTGCTCGGTGTGGAATGAGAGAGACACAGG 697
QY 963 TTTTCAAGCTTGTGTTTGGCCATATGATGTTCTTCTTCTGATGTGGCGCCCTACAATA 1022
Db 698 CTGTGAGGCTTATCTTCAACCATCATGATTGTTTATTTCTTCTGCGCTCCCTACAACA 757
QY 1023 TTGCATTTTCTGTGTCACCTTCAAGAACATTTCTCCCTGAGTGAGCTGCAAGAGAGCT 1082
Db 758 TTGTCTCTTCTGGAACACCTTCCAGGAATTTCTTTGGCCTGAAATTAATTGAGTAGCTCTA 817
QY 1083 ACAATCTGGAACAAAGTTTCAATCACTAACTCATCGCCACCCACCTGCTGTCATCA 1142
Db 818 ACAGTTGGACCAAGCTATGAGGTGACAGACTCTTTGGGATGACGCACTGCTGTCATCA 877
QY 1143 ACCCTCTCTGTATGCTTTCTTGTGAGGACATTTAGCAATACCTCTGCGCTGTTTCC 1202
Db 878 ACCCATCATCTATGCTTTGTGGGAGAGTTTCAGAACTACCTTCTTGTCTTCTTCC 937
QY 1203 ATCTGCGTAGTAACA 1217
Db 938 AAAAGCACATTTGCCA 952

RESULT 8

US-09-023-655-967
; Sequence 967, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 967:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1502408
; US-09-023-655-967

Query Match 13.6%; Score 230.6; DB 4; Length 1225;
Best Local Similarity 57.0%; Pred. No. 2.1e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGCAAGTATGACGCCAGGCACCTCTCAGCCAGCTGGTGCCATCACTCT 389
Db 76 CGGAGCCCTGCCAAAATAATCAATGTGAAGCAATCGAGCCCGCTCTCGCTCCGCTCT 135
QY 390 GCTCTGCTGTGTTGTGATCGGTGCTCTCGACAATCTCCTGGTGTGCTTATCTGTGTA 449
Db 136 ACTCACTGGTGTTCATCTTTGGTTTGGGCAACATGCTGGTCACTCTCATCTCTGATA 195
QY 450 AATATAAGAGCTCAAAACGGTGGAAATATCTATCTTCTTAACTTGGGAGTTTCTAACT 509
Db 196 ACTGCAAAAGGCTGAAGAGCACTGACATCTACCTGTCTCAACCTGGCCATCTCTGACC 255
QY 510 TGTGTTTCTGCTTACCTGCTCTGCTCATGCTGGGGCG----- 554
Db 256 TGTGTTTCTGCTTACTGCTGCTCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
QY 555 ---ATCCCATGTGTAATAATTCTCATTGGACTGTGCTGCTGCTGCTGCTGCTGCTGCT 611
Db 316 GAAATACAAATGTGCAACTCTTGACAGGCTCTATTTTATAGGCTCTCTCTCTGGAATCT 375
QY 612 TTTTCAATTTGCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTGGCAAGGGCACTTTT 671
Db 376 TCTTCATCATCTCTCTGACAAATCGATAGGTACTGCTGCTGCTGCTGCTGCTGCTGCT 435
QY 672 TCTCAGCCAGGAGGGTGCCTGTGGCATCAATACAAAGTGTCTCTGGCATGGTAAACAG 731
Db 436 TAAAGCC---AGGACGGTCACTTTGGGGTGTGACAGTGTGATGATGATGATGATGATG 492
QY 732 CCATTTCTGGCCACTTTTGCCTGAAATAGTGTGTTTATAAACTCAGATGGAAGACCAAGAA 791
Db 493 CTGTGTTTGGTCTCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAAGGTCTTCAAT 552
QY 792 ACAAGTGTGATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACATTTCTGAGAGCAT 851
Db 553 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 603
QY 852 TTCTGACTTTTAAATGAACATTTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db 604 TCAGACATTAAGATAGTATCTTTGGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
QY 912 TCTATGTGCAATGAGAAAAACACTA-----AGTTTCAGGGAGCAGAGGTATAGCC 962
Db 664 GCTACTCGGAATCTTAAACCTCTGCTTCCGTTGTCGAAATGAGAAAGAGAGCAGAGG 723
QY 963 TTTTCAAGCTTGTGTTTGGCCATTAAGGTAGTCTTCTCTGATGTGGGGCCCTACAATA 1022
Db 724 CTGTGAGGCTTATCTTCAACCATCATGATTTTATTTTCTTCTTCTGCGCTCCCTACAACA 783
QY 1023 TTGCATTTTCTGCTGCTCACTTTTCAAGAACACTTTCTCCCTGAGTGTGCAAGAGAGCT 1082
Db 784 TTGTCTCTCTCTGAAACACTTCCAGGAATTTCTTGGCCTGAAATAATTGAGTAGCTCTA 843
QY 1083 ACAATCTGGAACAAAGTGTTCATCACTCACTAACTCATCGCCACCCACTGCTGCTATCA 1142

Db 844 ACAGTTGACCAAGCTATGCGAGTGACAGACACTCTTGGGATGACGCACTCTGTCATCA 903
QY 1143 ACCCTCTCTGATGCGTTCTTGTGATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCC 1202
Db 904 ACCCATCATCTATGCTTTGTGCGGGAAGTTTCAGAAACTACCTCTTAGTCTTCTTCC 963
QY 1203 ATCTGCGTAGTAACA 1217
Db 964 AAAAGCACATTGCCA 978

RESULT 9
US-09-087-232A-12
; Sequence 12, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..1298
US-09-087-232A-12

Query Match 13.6%; Score 230.6; DB 3; Length 1376;
Best Local Similarity 57.0%; Pred. No. 2.2e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGACAAAGTATGACGCCGAGCACTCTCAGCCGAGCTGTGGCCATCACTCT 389
Db 289 CGGAGCCCTGCCAAAAATCAATGTGAAGCAAAATCGAGCCGCGCTCCTGCGCTCGCTCT 348
QY 390 GCTCTGCTGTTGTGATCGGTGCTCGGAAATCTCTGTTGTGCTTATCTCGGTAA 449
Db 349 ACTCACTGGTGTCTATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 408
QY 450 AATATAAGAGCTCAAAACGCTGGAAATATCTATCTTCTAACTTGGCAGTTTCTAACT 509

Db 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACTCTCAACCTGGCCATCTCTGTACC 468
QY 510 TGTGTTTCTTGTCTACCCCTGCTTCTGGGCTCATGCTGGGGGCG----- 554
Db 469 TGTGTTTCTTGTCTTACTGCTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTG 528
QY 555 ---ATCCCATCTGTGAAAAATTTCTATTGGACGTGTAATCTGTTGGGCTGTGACGTGAGACAT 611
Db 529 GAAATACAAATGTGCAACTCTTGACAGGGCTCTATTTTATAGGGCTCTTCTCTGGAATCT 588
QY 612 TTTTCAATTTGCTTCTGACTGTGCAAAAGGTACTAGTGTGTTTGTGCAAGGCAACTTTT 671
Db 589 TCTTCATCATCTCTCTGACAAATCGATAGTACCTGGCTGTCGTCTCATGCTGTGTTTGTCTT 648
QY 672 TCTCAGCCAGGAGGAGGTGCTGTCATCATTTACAAAGTGTCTGCGGATGGGTAAACAG 731
Db 649 TAAAGAGCC---AGGACGGTCACTTTGGGGTGGTGACAAAGTGTGATGATCACTTTGGTGGTGG 705
QY 732 CCATTCTGGCCACTTTGGCTGAATACGTTGTTTATAAACTCAGATGGAAGACCAAGAAAT 791
Db 706 CTGTGTTTGGCTCTCTCCAGGAATCATCTTTTACAGATCTCAAAAAGAAAGTCTTCAAT 765
QY 792 ACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGTGATGACAGACATTTCTGGAAGCAAT 851
Db 766 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 816
QY 852 TCTGACCTTTAAAAATGAACATTTTGGTCTTGTCTCCCTCATTTATTTTATTTTACATTTTC 911
Db 817 TCCAGACATTTAAAGATAGTATCTTGGGGCTGGTCTGCTCCGCTGCTTGTCTATGTTGTCATCT 876
QY 912 TCTATGTGCAATGAGAAACACTA-----AGTTTCAAGGAGGAGGATATAGCC 962
Db 877 GCTACTCGGGAATCTTAAAAAACTCTGCTTCCGTTGCGAAATGAGAAAGAGGACACAGG 936
QY 963 TTTTCAAGCTTGTGTTTGGCCATAATGTTAGTCTTCTCTGATGTTGGGCGCCCTACAAATA 1022
Db 937 CTGTGAGGCTTATCTTACCATCATGATGTTGTTATTTCTTCTTGGGCTCCCTACACA 996
QY 1023 TTGCAATTTTCTGTCTCACTTTTCAAGAACTTCTTCCCTGAGTGACATGCAAGAGCAGCT 1082
Db 997 TGTGCTTCTCTGAAACACCTTCCAGGAATTTCTTGGCTGCAATAATTTGCAAGTAGCTCTA 1056
QY 1083 ACAATCTGGACAAAGTGTTCACATCACTAACTATCGCCACCACTGCTGCTCATCA 1142
Db 1057 ACAGTTGGACCAAGCTATGACAGTATGACAGAGCTCTTGGGATGACGCACTGCTGCATCA 1116
QY 1143 ACCCTCTCTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCTCTGCGCTGTTTCC 1202
Db 1117 ACCCATCATCTATGCGCTTGTGCGGGAGAGTTTCAGAAACTACCTCTTAGTCTTCTTCC 1176
QY 1203 ATCTGCGTAGTAACA 1217
Db 1177 AAAAGCACATTGCCA 1191

RESULT 10
US-09-016-434-1104
; Sequence 1104, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; LIBRARY: GENBANK
; CLONE: G1262810
; US-09-016-434-1104

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Query Match      13.6%; Score 230.6; DB 4; Length 1376;
Best Local Similarity 57.0%; Pred. No. 2.2e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTGACAGTATGAGCCCGAGGACCTCTCAGCCAGCTGGTGCCATCACTCT 389
DB 289 CGAGGCCCTGCCAAAATAATCAATGTGAGCAATCGCAGCCCGCTCTCGCTCCGCTCT 348
QY 390 GCTCTGCTGTGTGTGATCGGTGCTCGGACAACTCTCTGGTGTGTGCTTATCCTGGTAA 449
DB 349 ACTCACTGTGTTCATCTTTGGTTTGTGGCAACATGCTGGTCACTCCTCATCTGATAA 408
QY 450 AATATAAGGACTCAACCGGTGGAAATATCTATCTTCTAACTTGGCAGTTTCTAACT 509
DB 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACC 468
QY 510 TGTGTTTCTGTCTACCTGCCCTTCTGGGCTCATGCTGGGGCG----- 554
DB 469 TGTGTTTCTGTCTACCTGCCCTTCTGGGCTCATGCTGGGGCG----- 528
QY 555 ----ATCCCATGTGTAATAATTTCTATTGGACTGTACTTCTGGGCTGTAGTGAGACAT 611
DB 529 GAAATACAATGTGCAACTCTTTGACAGGGCTCTATTTTATAGGCTTCTTCTCGGAATCT 588
QY 612 TTTTCAATTCCTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGTGCAAGGGCAACTTTT 671
DB 589 TCTTCATCATCTCTCGTCAATCGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
QY 672 TCTCAGCAGGAGGAGGGTCCCTGTGGCATCATTAACAAGTGTCTGGCATGGTAAACAG 731
DB 649 TAAAGGCC---AGGACGGTCACTTTGGGGTGGTGACAAAGTGTGATCACTTGGGTGGTG 705
QY 732 CCATCTGCGCCACTTTGCTGTAATAGTGTGTTTATTAACCTCAGATGGAAGACCAAT 791
DB 706 CTGTGTTTGGGCTCTCCAGGATCATCTTTACCAGATCTCAAAAGAGGTCTTCAAT 765
QY 792 ACAAGTGTGCAATTTAGCAGACTCCCTTCTGCGCAGCTGATGAGACATTTCTGGAAGCAAT 851
DB 766 ACACCT-----GCAGCTCTCAATTTTCCATACAGTCAGTATCAATTTCTGGAAT 816
QY 852 TTTGACTTTAAAGTGAACATTTCCGTTCTGTCTCCCTCATTTATTTTACATTTTC 911
DB 817 TCCAGACATTAAGATAGTCACTTTGGGGCTGGTCTCTGCGCTGTGTGTCATGGTCACTCT 876

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QY 912 TCTATGTGCAAAATGAGAAAAACACTA-----AGGTTTCAGGAGCAGAGGTATAGCC 962
DB 877 GCTACTCGGAATCTTAAAAACTCTGCTCGGTGTGAAATGAGAAAGGACACAGG 936
QY 963 TTTTCAAGCTGTGTTTGGCATAATGATAGTCTTCTTCTGTGATGTGGGCGCCCTTACAATA 1022
DB 937 CTGTGAGGCTTATCTTTCACCATCATGATGTTTATTTCTCTTCTGGGCTCCCTTACAACA 996
QY 1023 TTGCATTTTCTGTCCTCACTTTTCAAGAACACTTCTCCCTGAGTGTGCAAGAGCAGCT 1082
DB 997 TTGTCTTCTCTGGAACACCTTTCAGGAATTTCTTGGCCCTGAAATAATTGAGTAGCTCTA 1056
QY 1083 ACAATCTGGACAAAAGTGTTCACATCACTAAACTCATGCGCACACCACCTGCTGTCATCA 1142
DB 1057 ACAGTTTGGACCAAGCTATGCAAGTGCACAGACTCTTGGGATGACGCACTGCTGTCATCA 1116
QY 1143 ACCCTCTCTGTATGCGTTTCTTGTATGGGACATTTAGCAAAATACCTTGTGGCTGTTTCC 1202
DB 1117 ACCCATCATCTATGCTTTGTGGGAGAAATTGAGAACTACCTCTTAGTCTTCTTCTTCC 1176
QY 1203 ATCTGCGTAGTAACA 1217
DB 1177 AAAGCACATTGCCA 1191

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RESULT 11
US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: human
US-09-796-202-2

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Query Match      13.6%; Score 230.6; DB 4; Length 1376;
Best Local Similarity 57.0%; Pred. No. 2.2e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTGACAGTATGAGCCCGAGGACCTCTCAGCCAGCTGGTGCCATCACTCT 389
DB 289 CGAGGCCCTGCCAAAATAATCAATGTGAGCAATCGCAGCCCGCTCTCGCTCCGCTCT 348
QY 390 GCTCTGCTGTGTGTGATCGGTGCTCGGACAACTCTCTGGTGTGTGCTTATCCTGGTAA 449
DB 349 ACTCACTGTGTTCATCTTTGGTTTGTGGCAACATGCTGGTCACTCCTCATCTGATAA 408
QY 450 AATATAAGGACTCAACCGGTGGAAATATCTATCTTCTAACTTGGCAGTTTCTAACT 509
DB 409 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACC 468
QY 510 TGTGTTTCTGTCTACCTGCCCTTCTGGGCTCATGCTGGGGCG----- 554
DB 469 TGTGTTTCTGTCTACCTGCCCTTCTGGGCTCATGCTGGGGCG----- 528
QY 555 ----ATCCCATGTGTAATAATTTCTATTGGACTGTACTTCTGGGCTGTAGTGAGACAT 611
DB 529 GAAATACAATGTGCAACTCTTTGACAGGGCTCTATTTTATAGGCTTCTTCTCGGAATCT 588
QY 612 TTTTCAATTCCTCTGACTGTGCAAAAGGTACCTAGTGTGTTTGTGCAAGGGCAACTTTT 671
DB 589 TCTTCATCATCTCTCGTCAATCGATAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648

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QY 672 TCTCAGCCAGGAGGAGGTCCTGTGGCATCATTAAGTGTCTTGGCATGGGTAAACAG 731
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 649 TAAAGGCC---AGGACGGTCACTTTGGGGTGGTACAGTGTATCACTTTGGGTGGTGG 705
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QY 732 CCAATTTCTGGCCACTTTGGCTGAATACGTGGTTTATAAACCCTCAGATGGAAGACCAAGAAAT 791
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QY 706 CTGTGTTTGGCGTCTCTCCCGAGNATCACTTTACAGATCTCAAAAGNAGGTCTTCATT 765
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 792 ACAAGTGTGCATTTTAGCAAACTCCCTTCCGCCAGTGTATGAGACATTTCTGGAAGCAATT 851
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 766 ACACCT-----GCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAAAT 816
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QY 852 TTCTGACCTTAAATGAACATTTGGTCTTGTCTCTCCCTATTTATTTTACATTTTC 911
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QY 817 TCCAGACATTAAGATAGTATCTTTGGGGCTGGTCTGCCCTGTGTGTGTCATCT 876
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 912 TCTATGTCAAAATGAGAAAACACTA-----AGGTTCAAGGAGCAGAGGTATAGCC 962
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 877 GCTACTCGGGAATCTTAAATCTCTCTTCGGTGTGCGAATGAGAAGAGGACACAGG 936
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 963 TTTTCAAGCTGTTTTTGGCCATAATGTAGTCTTCTCTGTATGTGGGGCCCTACAATA 1022
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QY 937 CTGTGAGGCTATCTTCAACATCATGATGTTTATTTTCTCTCTGGGCTCCCTACAACA 996
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1023 TTGCATTTTCTGTCTCCACTTTCAAGAACACTTTCTCCCTGAGTGAAGTGCAGAGCAGCT 1082
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 997 TTGTCTCTCTCTGAACACTTTCCAGGAATTTTGGGCTGAATTAATGTCAGTATCTTA 1056
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QY 1083 ACAATCTGGACAAAAGTGTTCATCATCACTAAATCATGCCACCACTGCTGCATCA 1142
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1057 ACAGGTTGGACCAAGCTATGAGGTGACAGAGACTCTTGGGATGAGCACTGCTGCATCA 1116
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1143 ACCCTCTCTGTATGCTTTTGTATGGGACATTTAGCAAAATACCTCTGCCGCTGTTTCC 1202
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1117 ACCCATCATCTATGCTTTGTGGGGAGAGTTTCAGAAACTACCTCTTAGTCTTCTTCC 1176
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1203 ATCTGGTAGTAACA 1217
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1177 AAAAGCACATGGCCA 1191
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-502-783A-1
; Sequence 1, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
US-09-502-783A-1

Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62; Indels 39; Gaps 4;
Matches 522; Conservative 0; Mismatches 354;

QY 330 CAGAGCAATGTGACAGTATGACGCCAGGCACTCTCAGCCAGGCTGGTGCCATCACTCT 389
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QY 308 CGGAGCCCTGCCAAAAAATCAATGTGAAGCAAAATCGACGCCGCTCTCTGCTCCGCTCT 367
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QY 1023 TTGCATTTTCTGTCTCACTTTTCAAGAACACTTCTCCCTGAGTGAAGTGCAGAGCAGCT 1082
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 13
US-09-502-784A-1
; Sequence 1, Application US/09502784A
; Patent No. 6743594
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Methods of Screening Using Human G-Protein
; TITLE OF INVENTION: Chemokine Receptor HDNR10 (CCR5)
; FILE REFERENCE: 1488.1150005
; CURRENT APPLICATION NUMBER: US/09/502,784A

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; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION:
US-09-502-784A-1

Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGACAAATGATGAGCCAGGCACTCTCAGCCAGCTGGTGCCTACTCT 389
DB 308 CGGAGCCCTGCCAAAATCAATGTGAAGCAATCGCAGCCGCGCTCTCGCTCCGCTCT 367
QY 390 GCTCTGCTGTGTGTGATCGGTCTCGACAAATCTCTGGTGTGCTTATCTGTGTAA 449
DB 368 ACTCACTGTGTTCATCTTTGGTTTGTGGCAACATGCTGGTCACTCTCTGTATA 427
QY 450 AATATAAGGACTCAAAAGCGGTGAAATATCTATCTTTAAACTTGGCAGTTCTTAAC 509
DB 428 ACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACTGGCCATCTCTGACC 487
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DB 488 TGTGTTTCTTGTACCTTCCCTTCTGGGCTCATGCTGGGGG----- 547
QY 555 ---ATCCCATGTGTAAATTTCTCATTTGAGTGTACTTCTGGGCTGTACAGTGAGACAT 611
DB 548 GAAATACATGTGTCACTCTTGACAGGGCTCTATTTTATAGGCTTCTCTGGATCT 607
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QY 672 TCTCAGCAGGAGGAGGTGCGCTGTGGCATCATTAACAAGTGTCTGGCATGGGTAAACAG 731
DB 668 TAAAGCC---AGGACGGTCACTTTGGGGTGTGTGACAAAGTGTGATCACTTTGGGTGGT 724
QY 732 CCATTTGGGCACCTTTGGCCTGAATACGTGTTTATATAACCTCAGATGGAAGACAGAAAT 791
DB 725 CTGTGTTGGCTCTCTCCAGGATCATCTTTACCAGATCTCAAAAGAGGTCTTCAT 784
QY 792 ACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGCAATCTGGAAGCAT 851
DB 785 ACACCT-----GCAGCTCTCATTTCCATACAGTCACTAGTATCAATCTGGAAGAA 835
QY 852 TTTCTGACTTTTAAATGAACATTTTCGTTTCTTGTCTTCCCTCCCTTATTTTACATTT 911
DB 836 TCAGACATTTAAAGATAGTCACTTTGGGGTGTGTGCTGCGCTGCTTGTATGCTCATCT 895
QY 912 TCTATGTGCAATGAGAAAAACACTA-----AGTTTCAGGAGCAGAGTATAGCC 962
DB 896 GCTACTCGGAATCTTAAATCTGCTTGGTGTGCAATGAGAGAGAGGCAAGG 955
QY 963 TTTTCAAGCTTGTGTTTGGCATAATAGTACTTCTTCTGTGATGTGGGCGCCCTCAATA 1022
DB 956 CTGTGAGGCTTATCTTCAACCATCATGATGTTTATTTTCTTCTTGGCTCCCTCAACA 1015
QY 1023 TTGCATTTTCTGTCACACTTTCAAGAACACTTTCTCCCTGAGTGTGCTGCAAGAGAGCT 1082
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QY 1083 ACAATCTGGACAAAAGTTTCAATCACTAAACTCATCGCCACCCACTGCTGTCATCA 1142
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RESULT 14
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; Sequence 1, Application US/09339912A
; Patent No. 6759519
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-339-912A-1

Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;
QY 330 CAGAGCAATGTGACAAATGATGAGCCAGGCACTCTCAGCCAGCTGGTGCCTACTCT 389
DB 308 CGGAGCCCTGCCAAAATCAATGTGAAGCAATCGCAGCCGCGCTCTCGCTCCGCTCT 367
QY 390 GCTCTGCTGTGTGTGATCGGTCTCGACAAATCTCTGGTGTGCTTATCTGTGTAA 449
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Db 836 TCAGACATTAAGATAGTCACTTTGGGCTGCTCCTGCGCTGCTTGTATGGTCACT 895
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; Sequence 1, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artificial Sequence: Genomic
US-09-195-662A-1
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Query Match 13.6%; Score 230.6; DB 4; Length 1414;
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels 39; Gaps 4;

QY 330 CAGAGCAATGTACAGATGATACGCCAGGCACCTCTCAGCCAGCTGGTGCCATCACTCT 389
Db 308 CGAGGCCCTGCCAAAATAATCATGTGAAGCAATTCAGAGCCCGCTCTCGCTCGCTCT 367
QY 390 GCTCTGCTGTTGTGATCGGTGTCCTGGACAACTCTCTGTTGTGCTTATCTCGGTAA 449
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 12109378

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1468.4	86.5	1475	15	US-10-223-085-15
4	1468.4	86.5	1475	15	US-10-223-084-15
5	1468.4	86.5	1475	15	US-10-223-088-15
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7	1468.4	86.5	1475	15	US-10-223-087-15

ALIGNMENTS

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US-10-717-597-300

Sequence 300, Application US/10717597

Publication No. US20040110221A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Burczynski, Michael E.

APPLICANT: Twine, Natalie C.

APPLICANT: Dornier, Andrew J.

APPLICANT: Trepicchio, William L.

APPLICANT: Slonim, Donna K.

APPLICANT: Stover, Jennifer A.

TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS

FILE REFERENCE: AM101080L

CURRENT APPLICATION NUMBER: US/10717,597

CURRENT FILING DATE: 2003-11-21

PRIOR APPLICATION NUMBER: US 60/459,782

PRIOR FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US 60/427,982

PRIOR FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 4904

SOFTWARE: Patentin version 3.2

SEQ ID NO 300

LENGTH: 1698

TYPE: DNA

ORGANISM: Homo sapiens

US-10-717-597-300

Query Match 100.0%; Score 1698; DB 19; Length 1698;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1698; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	AGAGCGTTTCAGAGATCTCTCGAGGCCCTGGGGAGCTTTTCAGTACTTTTATTTTCAGTTGG	60
Db	1	AGAGCGTTTCAGAGATCTCTCGAGGCCCTGGGGAGCTTTTCAGTACTTTTATTTTCAGTTGG	60
Qy	61	TCCCTGAGCTCGGTGAGTGGGGCGGGTAGAGCCACAGGGGAATCAAACAGTGTGTTCTCG	120
Db	61	TCCCTGAGCTCGGTGAGTGGGGCGGGTAGAGCCACAGGGGAATCAAACAGTGTGTTCTCG	120
Qy	121	TGCCCCCTCAGGCTCAGAGCAGTCTGATCAAAAGGAGGCATCCACGTCCGGGGCCATT	180
Db	121	TGCCCCCTCAGGCTCAGAGCAGTCTGATCAAAAGGAGGCATCCACGTCCGGGGCCATT	180
Qy	181	CCACACGCTCCGGATCGTGGTCTGAGAGCTGGCCCTTCCCCTGCGAGGAGCTCAGCCC	240
Db	181	CCACACGCTCCGGATCGTGGTCTGAGAGCTGGCCCTTCCCCTGCGAGGAGCTCAGCCC	240
Qy	241	AGTGGGCACTCTGAAGATGGCCAAATTACACGCTGGCACACAGAGATGAATATGATGTCCT	300
Db	241	AGTGGGCACTCTGAAGATGGCCAAATTACACGCTGGCACACAGAGATGAATATGATGTCCT	300
Qy	301	CATAGAGGTGAACCTGAGAGCGATGAGGCAGACAGCAATGTGCAACGTATCACGCCACAGC	360
Db	301	CATAGAGGTGAACCTGAGAGCGATGAGGCAGACAGCAATGTGCAACGTATCACGCCACAGC	360
Qy	361	ACTCTCAGCCAGCTGGTGGCCATCACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	420
Db	361	ACTCTCAGCCAGCTGGTGGCCATCACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	420
Qy	421	CAATCTCCTCGTGTGTCTTATCTCTGGTAAATAATAAAGGACTCAACCGCTGGAAATAT	480
Db	421	CAATCTCCTCGTGTGTCTTATCTCTGGTAAATAATAAAGGACTCAACCGCTGGAAATAT	480
Qy	481	CTATCTTTCTAAACCTTGGCAGTTCTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540
Db	481	CTATCTTTCTAAACCTTGGCAGTTCTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540
Qy	541	TCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTGACTTCGTGGGCCGTGA	600
Db	541	TCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGACTGTGACTTCGTGGGCCGTGA	600
Qy	601	CAGTGAGACATTTTTCAATTTGCCCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTTCACAA	660
Db	601	CAGTGAGACATTTTTCAATTTGCCCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTTTCACAA	660
Qy	661	GGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTCTCTGGC	720
Db	661	GGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTCTCTGGC	720
Qy	721	ATGGGTAAACAGCCATCTCGCCACTTTGGCTCTGAATAGTGGTTTATAAACTCAGATGGA	780
Db	721	ATGGGTAAACAGCCATCTCGCCACTTTGGCTCTGAATAGTGGTTTATAAACTCAGATGGA	780
Qy	781	AGACGAGAAATACAAGTGTGCATTTAGCAGAACTCCCTCTCTGCCAGCTGATGAGACATT	840
Db	781	AGACGAGAAATACAAGTGTGCATTTAGCAGAACTCCCTCTCTGCCAGCTGATGAGACATT	840
Qy	841	CTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTGGTGTCTCTCTCTCTCTCTCTCTCT	900
Db	841	CTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTGGTGTCTCTCTCTCTCTCTCTCTCT	900
Qy	901	TTTTTACATTTCTCTATGTGCATATGAGAAACACTAAGCTTCAGGGAGCAGAGGTATAG	960
Db	901	TTTTTACATTTCTCTATGTGCATATGAGAAACACTAAGCTTCAGGGAGCAGAGGTATAG	960
Qy	961	CCTTTTCAAGCTGTTTTTGGCCATAATGTGTAGTCTTCTCTGATGTGGGGCCCTACAA	1020
Db	961	CCTTTTCAAGCTGTTTTTGGCCATAATGTGTAGTCTTCTCTGATGTGGGGCCCTACAA	1020
Qy	1021	TATGTCAATTTTCTCTGCCATTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAG	1080
Db	1021	TATGTCAATTTTCTCTGCCATTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAG	1080

RESULT 2

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US-10-741-600-13
; Sequence 13, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-13

```

Query Match	99.7%	Score 1693.6	DB 21	Length 1776
Best Local Similarity	99.4%	Pred. No. 0		
Matches 1687	Conservative	11	Mismatches 0	Indels 0
Gaps 0				
Qy	1	AGAGCTTCAGAGATCCTCTGGAGGCGCTGGGGGAGCTTTTCAGTACTTTATTTTCAGTTGG	60	
Db	72	AGAGCTTCAGAGATCCTCTGGAGGCGCTGGGGGAGCTTTTCAGTACTTTATTTTCAGTTGG	131	

Qy	61	TCCCTGAGCTCGGTAGTGGGGGGGTAGAGCCACGAGGGAAATCAACAGTGGTTTCTCG	120
Db	132	TCCCTGAGCTCGGTAGTGGGGGGGTAGAGCCACGAGGGAAATCAACAGTGGTTTCTCG	191
Qy	121	TGCCCCCTCAGGCTCAGGAGCAGTCTGATCAAAAGGAGGGCAATCCACTGTCCGGGGCCATT	180
Db	192	TGCCCCCTCAGGCTCAGGAGCAGTCTGATCAAAAGGAGGGCAATCCACTGTCCGGGGCCATT	251
Qy	181	CCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTCTCAGGAGCTCAGCCC	240
Db	252	CCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCTCTCAGGAGCTCAGCCC	311
Qy	241	AGTGGGAGTCTGAAGATGGCCAATTCACGCTGGCACACGAGAGTGAATATGATGTCCT	300
Db	312	AGTGGGAGTCTGAAGATGGCCAATTCACGCTGGCACACGAGAGTGAATATGATGTCCT	371
Qy	301	CATAGAAGGTGAATCGGAGAGCGATGAGGCAGAGCAATGTACAAAGTATGACGCCAGGC	360
Db	372	CATAGAAGGTGAATCGGAGAGCGATGAGGCAGAGCAATGTACAAAGTATGACGCCAGGC	431
Qy	361	ACTCTCAGCCAGCTGGTGCCATCACCTCTGCTGTGTCTGTGATCGGTGTCCTGGA	420
Db	432	ACTCTCAGCCAGCTGGTGCCATCACCTCTGCTGTGTCTGTGATCGGTGTCCTGGA	491
Qy	421	CAATCTCTGTTGTCTTATTCCTGGTAAATATATAAGGACTCAACCGCTGGAAATAT	480
Db	492	CAATCTCTGTTGTCTTATTCCTGGTAAATATATAAGGACTCAACCGCTGGAAATAT	551
Qy	481	CTATCTTTCAAACTTGGCAGTTTCTAACTTGTGTCTTCTGCTTACCTGCTCCTGCGGC	540
Db	552	CTATCTTTCAAACTTGGCAGTTTCTAACTTGTGTCTTCTGCTTACCTGCTCCTGCGGC	611
Qy	541	TCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCGCTGTA	600
Db	612	TCATGCTGKGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGCGCTGTA	671
Qy	601	CAGTGAGACATTTTTTCAATTGCCCTTCTGACTGTGCAAGGTACTAGTGTTTTGCAAA	660
Db	672	CAGTGAGACATTTTTTCAATTGCCCTTCTGACTGTGCAAGGTACTAGTGTTTTGCAAA	731
Qy	661	GGGCAACTTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTCTGGC	720
Db	732	GGGNAACTTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTAAGTGTCTGGC	791
Qy	721	ATGGGTAAACAGCCATCTCGGCCACTTTGCGCTGAATAGTGGTTTATAAACCTCAGATGGA	780
Db	792	ATGGGTAAACAGCCATCTCGGCCACTTTGCGCTGAATAGTGGTTTATAAACCTCAGATGGA	851
Qy	781	AGACCAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATT	840
Db	852	AGACCAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCGAGCTGATGAGACATT	911
Qy	841	CTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTCCGTTCTGTGCTCCCTCTTTTAT	900
Db	912	CTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTCCGTTCTGTGCTCCCTCTTTTAT	971
Qy	901	TTTTTACATTTCTCTATGTGCAATTGAGAAAAACACTAAGGTTCAAGGAGCAGAGGTATAG	960
Db	972	TTTTTACATTTCTCTATGTGCAATTGAGAAAAACACTAAGGTTCAAGGAGCAGAGGTATAG	1031
Qy	961	CCTTTTCAAGCTGTTTTTGGCCATAATGGTAGTCTTCTCTGATGTGGCGCCCTACAA	1020
Db	1032	CCTTTTCAAGCTGTTTTTGGCCRTAATGGTAGTCTTCTCTGATGTGGCGCCCTACAA	1091
Qy	1021	TATTTGCATTTTCTCTGTCCATTTCAAAGAACACTTCTCCCTGTAGTGACTGCAAGAGCAG	1080
Db	1092	TATTTGCATTTTCTCTGTCCATTTCAAAGAACACTTCTCCCTGTAGTGACTGCAAGAGCAG	1151
Qy	1081	CTACAACTCTGACAAAAAGTGTTCACATCCTATAACTCATGCCACCACCTGCTGTCAT	1140
Db	1152	CTACAACTCTGACAAAAAGTGTTCACATCCTATAACTCATGCCACCACCTGCTGTCAT	1211
Qy	1141	CAACCCCTCTCCTGTATCGGTTTCTTGATGGGACATTTTAGCAAAATPACCTCTGCCGCTGTTT	1200

RESULT 3

RESULTS
US-10-223-085-15

US-10-223-063-13
: Sequence 15. Application us/102233085

Sequence 13, Application US/102
; Publication No. US20030100497A1

: PUBLICATION NO. US20
: GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James

; APPLICANT: Stephan, Jean-Phil

; APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

```

; APPLICANT: Williams,
: APPLICANT: VO Weilan

```

APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P3235P1C10

; FILE REFERENCE: P3235PIC10
; CURRENT APPLICATION NUMBER: US/1

; CURRENT APPLICATION NUMBER: US/10/223,0
 : CURRENT FILING DATE: 2002-08-16

; CURRENT FILING DATE: 2002-08-
 : PRIOR APPLICATION NUMBER: US 1

; ERROR AFFILIATION NUMBER: 03 10/081,030
 : PRIOR FILING DATE: 2002-02-20

; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 6

PRIOR FILING DATE: 2000-06-23

; PRIORITY APPLICATION NUMBER: US 6

PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 6

```
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-085-15

Query Match      86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACGAGAGATGA 288
DB 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACGAGAGATGA 60
QY 289 ATATGATGTCTCATAGAAAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAAGTA 348
DB 61 ATATGATGTCTCATAGAAAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAAGTA 120
QY 349 TGACGCCAGGCACTCTACGCCAGCTGTGCGCATCACTCTGCTGTGCTGTGTTGTGAT 408
DB 121 TGACGCCAGGCACTCTACGCCAGCTGTGCGCATCACTCTGCTGTGCTGTGTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCTGTTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAGC 468
DB 181 CGGTGTCCTGGCAATCTCTGTTGTGCTTATCTCTGGTAAATATAAAGGACTCAAAGC 240
QY 469 CGTGAAATATCTATCTTTCTAAACTTGGCAGTTCCTAACTTGTGTTCTTCTTACCCCT 528
DB 241 CGTGAAATATCTATCTTTCTAAACTTGGCAGTTCCTAACTTGTGTTCTTCTTACCCCT 300
QY 529 GGCCTCTGGCTCATGCTGGGGGCGATCCCATGTGTAAATCTCATTTGAGCTGACTT 588
DB 301 GGCCTCTGGGCTCATGCTGGGGGCGATCCCATGTGTAAATCTCATTTGAGCTGACTT 360
QY 589 CGTGGSCCTGTACAGTGAGACATTTTCAATTCCTCTGACTGTGCAAGGTACTAGT 648
DB 361 CGTGGSCCTGTACAGTGAGACATTTTCAATTCCTCTGACTGTGCAAGGTACTAGT 420
QY 649 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 708
DB 421 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCATTTAC 480
QY 709 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTTGGCTGAAATAGCTGTTTATAA 768
DB 481 AAGTGTCTGGCATGGTAAAGCCATTTCTGGCCACTTTTGGCTGAAATAGCTGTTTATAA 540
QY 769 ACTCAGATGGAAGACACGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGC 828
DB 541 ACTCAGATGGAAGACACGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGC 600
QY 829 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTCTGTTCTCT 888
DB 601 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTCTGTTCTCT 660
QY 889 CCCCCTATTATTTTACATTTCTCTATGTGCAATAGAAAAACACATAGGTTTCAGGA 948
DB 661 CCCCCTATTATTTTACATTTCTCTATGTGCAATAGAAAAACACATAGGTTTCAGGA 720
QY 949 GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTTCGCATATAGGTAGTCTTCTCTGATGTG 1008
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DB 721 GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTTCGCATATAGGTAGTCTTCTCTGATGTG 780
QY 1009 GCGCCCTTACAAATATTTGCAATTTTCTGTCACATTTTCAAGAAACACTTCTCTCGAGTGA 1068
DB 781 GCGCCCTTACAAATATTTGCAATTTTCTGTCACATTTTCAAGAAACACTTCTCTCGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACCAC 1128
DB 841 CTGCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACATCACTAACTCATCGCCACCAC 900
QY 1129 CCACGTGTCATCAACCCCTCTCTGTATGCGTTCCTGATGGGACATTTAGCAAAATACCT 1188
DB 901 CCACGTGTCATCAACCCCTCTCTGTATGCGTTCCTGATGGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACA 1248
DB 961 CTGCGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACA 1020
QY 1249 AGGCATCTGAGGGAAGCACTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1308
DB 1021 AGGCATCTGAGGGAAGCACTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1080
QY 1309 GCAAGAAATATAACATGGAATTTTTCATCTTCTGCAATTTTCAATGTAAATTTTCTACAC 1368
DB 1081 GCAAGAAATATAACATGGAATTTTTCATCTTCTGCAATTTTCAATGTAAATTTTCTACAC 1140
QY 1369 ATTTGTATACAAATTCGGATACAGAAAGGAGAGGTGAGTAACTATTTGCTTAAGC 1428
DB 1141 ATTTGTATACAAATTCGGATACAGAAAGGAGAGGTGAGTAACTATTTGCTTAAGC 1200
QY 1429 ACTGAAATTTGCTCAGGCAACCGTCAAGGCTTTTACAAAGTGTAGCTTCTCGCTCCT 1488
DB 1201 ACTGAAATTTGCTCAGGCAACCGTCAAGGCTTTTACAAAGTGTAGCTTCTCGCTCCT 1260
QY 1489 ACCACTTCTCCTAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAACTAAGGCG 1548
DB 1261 ACCACTTCTCCTAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAACTAAGGCG 1320
QY 1549 CGGAAATTTGCTTAAGATCATTAACTAGGAGTGGGAGAACTGATTTCTCGAGCCCTGCT 1608
DB 1321 CGGAAATTTGCTTAAGATCATTAACTAGGAGTGGGAGAACTGATTTCTCGAGCCCTGCT 1380
QY 1609 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCCCTGGGACAAA 1668
DB 1381 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCCCTGGGACAAA 1440
QY 1669 GCACATGAAATAAATGTATTTTAAACATC 1698
DB 1441 GCACATGAAATAAATGTATTTTAAACATC 1470
```

RESULT 4

US-10-223-084-15

; Sequence 15, Application US/10223084

; Publication No. US20030105011A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Masters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Stephan, Jean-Philippe P.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

;; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

;; FILE REFERENCE: P3235P1CS
;; CURRENT APPLICATION NUMBER: US/10/223,084
;; CURRENT FILING DATE: 2002-08-16
;; PRIOR APPLICATION NUMBER: US 10/081,056
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/213,637
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: US 60/219,556
;; PRIOR FILING DATE: 2000-07-20
;; PRIOR APPLICATION NUMBER: US 60/220,624
;; PRIOR FILING DATE: 2000-07-25
;; PRIOR APPLICATION NUMBER: US 60/220,664
;; PRIOR FILING DATE: 2000-07-25
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 60/222,695
;; PRIOR FILING DATE: 2000-08-02
;; PRIOR APPLICATION NUMBER: US 09/643,657
;; PRIOR FILING DATE: 2000-08-17
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 383
;; SEQ ID NO 15
;; LENGTH: 1475
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-223-084-15

Query Match 86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	229	GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACACGCTGGCCACGAGGATGA	288
DB	1	GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATACACGCTGGCCACGAGGATGA	60
QY	289	ATATGATGCTCTATAGAGGTGAATGGAGCGGATGAGGAGGCAATGTGCAAGTA	348
DB	61	ATATGATGCTCTATAGAGGTGAATGGAGCGGATGAGGAGGCAATGTGCAAGTA	120
QY	349	TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTCTGAT	408
DB	121	TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTCTGAT	180
QY	409	CGGTGTCTGGCAATCTCTCTGTTGTGCTTTATCTCTGGTAAATATAAAGGACTCAAACG	468
DB	181	CGGTGTCTGGCAATCTCTCTGTTGTGCTTTATCTCTGGTAAATATAAAGGACTCAAACG	240
QY	469	CGTGGAATAATCTATCTCTAACTTGGCAGTTTCTAACTTGATGTTTCTTGCTTACCT	528
DB	241	CGTGGAATAATCTATCTCTAACTTGGCAGTTTCTAACTTGATGTTTCTTGCTTACCT	300
QY	529	GCCTTTCTGGCTCATCTGGGGGCGATCCCATGTGTAATTTCTCATTTGGCTGACT	588
DB	301	GCCTTTCTGGCTCATCTGGGGGCGATCCCATGTGTAATTTCTCATTTGGCTGACT	360
QY	589	CGTGGGCTGTACAGTGAGACATTTTTCATTTCAATTGCTTCTGACTGTGCAAGGTAACCTAGT	648
DB	361	CGTGGGCTGTACAGTGAGACATTTTTCATTTGCTTCTGACTGTGCAAGGTAACCTAGT	420
QY	649	GTTTTGGCAAGGGCAATTTTTCACCGAGGAGGGTGCCTGTGGCATCATTTAC	708
DB	421	GTTTTGGCAAGGGCAATTTTTCACCGAGGAGGGTGCCTGTGGCATCATTTAC	480
QY	709	AAAGTGCTGGGATGGTAAACAGCCATTCTGGCCACTTTGCCCTGATAGCTGGTTATAA	768
DB	481	AAAGTGCTGGGATGGTAAACAGCCATTCTGGCCACTTTGCCCTGATAGCTGGTTATAA	540
QY	769	ACCTCAGATGGAAGACCAAGAAATACAAAGTGTGCATTTAGCAGAACTCCCTTCTCTGCCAGC	828

DB	541	ACCTCAGATGGAAGACCAAGATGCAATTTAGCAGAACTCCCTTCTCTGCCAGC	600
QY	829	TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACTTTGGTCTTGTCT	888
DB	601	TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACTTTGGTCTTGTCT	660
QY	889	CCCCCTATTATTTTATACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGA	948
DB	661	CCCCCTATTATTTTATACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGA	720
QY	949	GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTGTATGTG	1008
DB	721	GCAGAGGTATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTGTATGTG	780
QY	1009	GGCGCCCTACAAATATTTGCAATTTTCTGTGTCACCTTTCAAAGAACACTTTCTCCCTGAGTGA	1068
DB	781	GGCGCCCTACAAATATTTGCAATTTTCTGTGTCACCTTTCAAAGAACACTTTCTCCCTGAGTGA	840
QY	1069	CTGCAAGAGCAGCTACAATCTGGACAAAAGTGTTCACATCAGTAACTCATGCGCACAC	1128
DB	841	CTGCAAGAGCAGCTACAATCTGGACAAAAGTGTTCACATCAGTAACTCATGCGCACAC	900
QY	1129	CCACTGCTGCATCAACCCCTCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCT	1188
DB	901	CCACTGCTGCATCAACCCCTCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCT	960
QY	1189	CTGCGCGCTGTTTCCATCTCGGTAGTAAACACCCACCTTCAACCCAGGGGGCAGTCTGCACA	1248
DB	961	CTGCGCGCTGTTTCCATCTCGGTAGTAAACACCCACCTTCAACCCAGGGGGCAGTCTGCACA	1020
QY	1249	AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT	1308
DB	1021	AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATCCACCAAT	1080
QY	1309	GCAAGAAGAAATAAACAATGGATTTTTCATCTTCTGCAATTAATTTTCATGTAAATTTTCTACAC	1368
DB	1081	GCAAGAAGAAATAAACAATGGATTTTTCATCTTCTGCAATTAATTTTCATGTAAATTTTCTACAC	1140
QY	1369	ATTGTTATACAAATTCGGATACAGGAAAGAGGAGAGGTGAGCTAACTTTGCTTAAGC	1428
DB	1141	ATTGTTATACAAATTCGGATACAGGAAAGAGGAGAGGTGAGCTAACTTTGCTTAAGC	1200
QY	1429	ACTGAATTTGCTCAGGACCGTGCAGAGCTCTTTTACAAACGTTAGCTCTTCCGCTCTCT	1488
DB	1201	ACTGAATTTGCTCAGGACCGTGCAGAGCTCTTTTACAAACGTTAGCTCTTCCGCTCTCT	1260
QY	1489	ACCACCTTGTCCATAGTGTGGATAGGACTAGTCTCTCATTTCTCTGAGAAAGAAACTAAAGCG	1548
DB	1261	ACCACCTTGTCCATAGTGTGGATAGGACTAGTCTCTCATTTCTCTGAGAAAGAAACTAAAGCG	1320
QY	1549	CGGAAATTTGCTTAAGATCACCTTAATAGGAAAGTGGAGAACTGATTTCCAGCCCTGGT	1608
DB	1321	CGGAAATTTGCTTAAGATCACCTTAATAGGAAAGTGGAGAACTGATTTCCAGCCCTGGT	1380
QY	1609	AGCATTTGCTCAGAGCTACGCTTGGTCCAGAACACTCAAACTCCAAACCTCGGGGCAAA	1668
DB	1381	AGCATTTGCTCAGAGCTACGCTTGGTCCAGAACACTCAAACTCCAAACCTCGGGGCAAA	1440
QY	1669	CGCATGAAATAAATGATTTTAAACATC	1698
DB	1441	CGCATGAAATAAATGATTTTAAACATC	1470

RESULT 5

US-10-223-088-15
; Sequence 15, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC6
; CURRENT APPLICATION NUMBER: US 10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-223-088-15

Query Match      86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCCACGAGGATGA 288
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QY 289 ATATGATGTCTCATAGAAAGTGAACTGGAGAGCGATGAGGAGAGCAATGTGACAAGTA 348
D 61 ATATGATGTCTCATAGAAAGTGAACTGGAGAGCGATGAGGAGAGCAATGTGACAAGTA 120
QY 349 TGACGCCACAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGTGTTGTGTGAT 408
D 121 TGACGCCACAGGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTCTGTGTTGTGTGAT 180
QY 409 CGGTGTCTGGACAATCTCTGTTGTGCTTATCTCTGGTAAATAATAAGGACTCAAAAG 468
D 181 CGGTGTCTGGACAATCTCTGTTGTGCTTATCTCTGGTAAATAATAAGGACTCAAAAG 240
QY 469 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTCTTCTAACTTGTGTCTTCTTACCCCT 528
D 241 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTCTTCTAACTTGTGTCTTCTTACCCCT 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGGGGATCCCATGTGTGTAATAATCTCATTTGGACTGTACTT 588
D 301 GCCCTTCTGGGCTCATGCTGGGGGGGATCCCATGTGTGTAATAATCTCATTTGGACTGTACTT 360
QY 589 CGTGGGCGCTGTACAGTGAGACATTTTTCATTTGCCTTCTGACTGTGCAAAAGGTACCTAGT 648

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421 GTTTTGTGCACAAGGGCAACTTTTCTCAGCCAGGAGGAGGGTGCCTCTGTGGCATCATTTAC 480
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481 AAGTGTCTCGCATGGGTAAACAGCCATTTCTGGCCACTTTTGCCTGTAATAGTGTGTTTATAA 540
769 ACCTCAGATGGAAGACCAAGAAATCAAGTGTGCAATTTAGCAGAACTCCCTCTCTGCCAGC 828
541 ACCTCAGATGGAAGACCAAGAAATCAAGTGTGCAATTTAGCAGAACTCCCTCTCTGCCAGC 600
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901 CCACCTGTGCAATCAACCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACCT 960
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1609 AGCATTTGCTCAGAGCTTACGCTTGGTCCAGAACTCAAACTCCAAACCCCTGGGACAAA 1668
1381 AGCATTTGCTCAGAGCTTACGCTTGGTCCAGAACTCAAACTCCAAACCCCTGGGACAAA 1440
1669 CGACATGAAATAAATGATTTTAAAAACATC 1698
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Db 1441 CGACATGAATAAATGATTATTTAAACATC 1470
RESULT 6
US-10-223-090-15
; Sequence 15, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-090-15
Query Match 86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 229 GGAGCTCAGCCAGTGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACAGAGGATGA 288
Db 1 GGAGCTCAGCCAGTGGCGAGTCTGAAGATGGCCAAATTACACGCTGGCACAGAGGATGA 60
QY 289 ATATGATGCTCATAGAGGTGAATCTGGAGAGCGGATGAGGAGAGCAATGTGCAAGTA 348
Db 61 ATATGATGCTCATAGAGGTGAATCTGGAGAGCGGATGAGGAGAGCAATGTGCAAGTA 120
QY 349 TGACGCCCGAGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTGCTGTTGTTGAT 408
Db 121 TGACGCCCGAGCACTCTCAGCCAGCTGGTGCCATCACTCTGCTGCTGTTGTTGAT 180
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181 CGGTGCTCTGGACAATCTCTGTTGTTGTTTCTCTGTTGTTTAAATATAAAGGACTCAACG 240
469 CGTGGAAATATCTATCTTTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCT 528
241 CGTGGAAATATCTATCTTTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGTCTTACCT 300
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301 GCCCTTCTGGGCTCATGCTGGGGCGCATCCATGTGTAAATTTCTCATTTGGACTGTACTT 360
589 CGTGGGCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAAAGGTACTTACT 648
361 CGTGGGCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAAAGGTACTTACT 420
649 GTTTTTGCAACAGGGCAACTTTTCTCAGCCAGGAGGAGGTCCTCTGTTGGCATCATTAC 708
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1009 GGGGCCCTACATATTGCAATTTTCTGTCCTCTTCAAGAACACTTCTCCCTCTGATGTA 1068
781 GGGGCCCTACATATTGCAATTTTCTGTCCTCTTCAAGAACACTTCTCCCTCTGATGTA 840
1069 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAAATCTATCGCCACAC 1128
841 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCACTAAATCTATCGCCACAC 900
1129 CCACTGCTGCATCAACCCCTCTCTCTGATGCGTTTCTTGTATGGACATTTAGCAAAATACCT 1188
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1369 ATTTGTATACAAATTCGATACAGGAGGAGGAGGAGTGTAGCTTAACATTTGCTAAGC 1428
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Db 1261 ACCACTTGTCATAGTGTGGATAGGACTAGTCTCATTTTCTCTGAGAAGAAACTAAGGCG 1320
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Db 1381 AGCATTTGCTCAGAGCTAGCTTGGTCCAGAACATCAAACTCCAAACCTCGGGGACAAA 1440
Qy 1669 CGCATGAATAAATGATTTTAAACATC 1698
Db 1441 CGCATGAATAAATGATTTTAAACATC 1470

RESULT 7
US-10-223-087-15
; Sequence 15, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; CURRENT APPLICATION NUMBER: US/10/223,087
; FILE REFERENCE: P3235P1C4
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
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; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
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; PRIOR APPLICATION NUMBER: US 09/866,028
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; PRIOR APPLICATION NUMBER: US 09/870,574
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; PRIOR APPLICATION NUMBER: PCT/US01/17443
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; PRIOR APPLICATION NUMBER: PCT/US01/19692
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; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-087-15
Query Match 86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 229 GGAGCTCAGCCAGTGGGCAGTCTGAAGATGGCCCAATTACAGCTGGCACCAGAGATGA 288
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Qy 1369 ATTTGTATACAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAAATTTGTCTAAGC 1428
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Qy 1549 CGGAAATTTGCTCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGT 1608
Db 1321 CGGAAATTTGCTCTAAGATCACTAATACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGGT 1380
Qy 1609 AGCATTTGCTCAGAGCCTAGCTTTGGTCCAGAAACATCAAACTCCAAACCCCTGGGGACAAA 1668
Db 1381 AGCATTTGCTCAGAGCCTAGCTTTGGTCCAGAAACATCAAACTCCAAACCCCTGGGGACAAA 1440
Qy 1669 CGACATGAAATAAATGATTTTAAACATC 1698
Db 1441 CGACATGAAATAAATGATTTTAAACATC 1470

RESULT 8

US-10-223-083-15
; Sequence 15, Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-083-15

Query Match 86.5%; Score 1468.4; DB 15; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 229 GGAGCTCAGCCCGAGTGGGCGAGTCTGAAGATGGCCAAATTACAGCTGGCACCGAGATGA 288
Db 1 GGAGCTCAGCCCGAGTGGGCGAGTCTGAAGATGGCCAAATTACAGCTGGCACCGAGATGA 60

QY 289 ATATGATGTCCTCATAGAGAGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAGTA 348
DB 61 ATATGATGTCCTCATAGAGAGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGTGGCCATCAGCTCTGCTGTGCTGTGTTGTGAT 408
DB 121 TGACGCCAGGCACTCTCAGCCAGCTGTGGCCATCAGCTCTGCTGTGCTGTGTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCTCTGTTGTGTTATCTCTGGTAAATATAAAGGACTCAAAAG 468
DB 181 CGGTGTCCTGGCAATCTCTCTGTTGTGTTATCTCTGGTAAATATAAAGGACTCAAAAG 240
QY 469 CGTGGAATATCTATCTCTAAACCTGGAGTTCTTAACCTGTGTTCTCTGCTTACCT 528
DB 241 CGTGGAATATCTATCTCTAAACCTGGAGTTCTTAACCTGTGTTCTCTGCTTACCT 300
QY 529 GCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGAGCTGACT 588
DB 301 GCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAATAATCTCATTTGGAGCTGACT 360
QY 589 CGTGGCCCTGTACAGTGAGACATTTTCAATTCGCTTCTGACTGTGCAAGGTACTAGT 648
DB 361 CGTGGCCCTGTACAGTGAGACATTTTCAATTCGCTTCTGACTGTGCAAGGTACTAGT 420
QY 649 GTTTTGGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCTATAC 708
DB 421 GTTTTGGCAAGGGCAACTTTTCTCAGCCAGGAGGGTGCCTGTGGCATCTATAC 480
QY 709 AAGTGTCTGGCATGGTAAACAGCCATCTCGGCCACTTTTGCCTGTAATAGTGTATATAA 768
DB 481 AAGTGTCTGGCATGGTAAACAGCCATCTCGGCCACTTTTGCCTGTAATAGTGTATATAA 540
QY 769 ACCTCAGATGGAAGACCAAGATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGC 828
DB 541 ACCTCAGATGGAAGACCAAGATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGC 600
QY 829 TGATGAGACATCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTGGTTCTGTCT 888
DB 601 TGATGAGACATCTGGAAGCATTTTCTGACTTTAAATAATGAACATTTGGTTCTGTCT 660
QY 889 CCCCCTATTTATTTTACATTTCTCTATGTGCAATGAGAAACACAACTAGGTTCAGGA 948
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QY 949 CGAGAGGTATAGCTTTTCAAGCTTTTGGCATAATGGTAGTCTTCTCTGATGTG 1008
DB 721 CGAGAGGTATAGCTTTTCAAGCTTTTGGCATAATGGTAGTCTTCTCTGATGTG 780
QY 1009 GGGGCCCTACATATTTGCAATTTTCTGTGCCATTTCAAGAACACTTCTCCCTGAGTA 1068
DB 781 GGGGCCCTACATATTTGCAATTTTCTGTGCCATTTCAAGAACACTTCTCCCTGAGTA 840
QY 1069 CTGCAAGAGCAGCTACAACTCTGACAAAGTGTTCACATCACTAACTCATGCCACCAC 1128
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QY 1129 CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAATACCT 1188
DB 901 CCACTGCTGCATCAACCCCTCTCTGTATGCGTTTCTTGATGGACATTTAGCAATACCT 960
QY 1189 CTGCGCTGTTTCCATCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1248
DB 961 CTGCGCTGTTTCCATCTGCTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1020
QY 1249 AGGCACATCGAGGAGAACCTTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1308
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QY 1309 GCAAGAAGATAAACATGATTTTCACTTTCTGCAATATTTTCACTGATAATTTTCTACAC 1368
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RESULT 9

US-10-223-089-15
; Sequence 15, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PLC9
; CURRENT APPLICATION NUMBER: US/10/223,089
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15

Query Match
Best Local Similarity 86.58; Score 1468.4; DB 15; Length 1475;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-223-089-15

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RESULT 10

US-10-223-081-15
Sequence 15, Application US/10223081
Publication No. US20030186866A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PIC7
CURRENT APPLICATION NUMBER: US/10/223,081
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710


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; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-081-15

Query Match      86.5%; Score 1468.4; DB 16; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCCGAGTGGGCGAGTCTGAAGATGGCCCAATTACACGCTGGCCACGAGGATGA 288
Db 1 CGAGCTCAGCCCGAGTGGGCGAGTCTGAAGATGGCCCAATTACACGCTGGCCACGAGGATGA 60
QY 289 ATATGATGTCCTCATAGAAAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAAGTA 348
Db 61 ATATGATGTCCTCATAGAAAGGTGAACCTGGAGAGCGATGAGGAGAGCAATGTGACAAGTA 120
QY 349 TGACGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCATCAGCTCTGCTGCTGCTGTTGTGAT 408
Db 121 TGACGCCCGAGGCACTCTCAGCCCGAGCTGGTGCCATCAGCTCTGCTGCTGCTGTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
Db 181 CGGTGTCCTGGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 469 CGTGGAAATATCTATCTTCTAAACTGGCAGTTCTAACTGTTCTAACTGTTCTGCTGCTGCT 528
Db 241 CGTGGAAATATCTATCTTCTAAACTGGCAGTTCTAACTGTTCTGCTGCTGCTGCTGCTGCT 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGGGGATCCCATGTGTAATAATCTCATTTGAGACTGACTT 588
Db 301 GCCCTTCTGGGCTCATGCTGGGGGGGATCCCATGTGTAATAATCTCATTTGAGACTGACTT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTTCATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
Db 361 CGTGGGCTGTACAGTGAGACATTTTTCATATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 649 GTTTTGGCAAGGGCACTTTTCTCAGCCAGGAGGAGGTCCTGTCGATCATTTAC 708
Db 421 GTTTTGGCAAGGGCACTTTTCTCAGCCAGGAGGAGGTCCTGTCGATCATTTAC 480
QY 709 AAGTGTCTGGGATGGGTAAACAGCCATCTGCGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db 481 AAGTGTCTGGGATGGGTAAACAGCCATCTGCGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 769 ACTCAGATGGAAGACCAAGATACAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
Db 541 ACTCAGATGGAAGACCAAGATACAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 829 TGATGAGACATCTGGAAGCACTTTCTGACTTTTAAATGAACATTTGGTTCTTGCTCT 888
Db 601 TGATGAGACATCTGGAAGCACTTTCTGACTTTTAAATGAACATTTGGTTCTTGCTCT 660
QY 889 CCCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAAAACAACTAAGGTTGAGGGA 948
Db 661 CCCCCTATTATTTTACATTTCTCTATGTGCAATGAGAAAAACAACTAAGGTTGAGGGA 720
QY 949 GCAGAGGTATAGCCTTTTCAAGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
Db 721 GCAGAGGTATAGCCTTTTCAAGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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QY 1009 GCGCGCCCTACAAATATTGCAATTTTCTCTCCACTTTTCAAGAAACACTTCTCCTCCTGAGTGA 1068
Db 781 GCGCGCCCTACAAATATTGCAATTTTCTCTCCACTTTTCAAGAAACACTTCTCCTCCTGAGTGA 840
QY 1069 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCATCTAAACTCATGCCACAC 1128
Db 841 CTGCAAGAGCAGCTACAAATCTGGACAAAAGTGTTCACATCATCTAAACTCATGCCACAC 900
QY 1129 CCATGCTGCAATCAACCCCTCTCTCTGATGCGTTTCTGATGCGGACATTTAGCAAAATACCT 1188
Db 901 CCATGCTGCAATCAACCCCTCTCTCTGATGCGTTTCTGATGCGGACATTTAGCAAAATACCT 960
QY 1189 CTGCGCGCTGTTTCCCATCTGCGTAGTAACACCCCACTTCAACCCGAGGAGCTGTCGACA 1248
Db 961 CTGCGCGCTGTTTCCCATCTGCGTAGTAACACCCCACTTCAACCCGAGGAGCTGTCGACA 1020
QY 1249 AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1308
Db 1021 AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACCAAT 1080
QY 1309 GCAAGAGAATAAACAATGGAATTTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1368
Db 1081 GCAAGAGAATAAACAATGGAATTTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1140
QY 1369 ATTTGTATACAAATCGGATACAGAAAGGAGAGGTGAGCTAACATTTGCTAAGC 1428
Db 1141 ATTTGTATACAAATCGGATACAGAAAGGAGAGGTGAGCTAACATTTGCTAAGC 1200
QY 1429 ACTGAATTTGCTCAGGCAACGCTGCAAGGCTCTTTTACAAAGTGTAGCTCTTCGCTCTCT 1488
Db 1201 ACTGAATTTGCTCAGGCAACGCTGCAAGGCTCTTTTACAAAGTGTAGCTCTTCGCTCTCT 1260
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Db 1381 AGCATTTGCTCAGAGCCTACGCTTGCTCCAGAACATCAAACTCCAAACCTTGGGGACAAA 1440
QY 1669 CGACATGAATAAATGTAATTTTAAACATC 1698
Db 1441 CGACATGAATAAATGTAATTTTAAACATC 1470
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RESULT 11

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US-10-223-082-15
; Sequence 15, Application US/10223082
; Publication No. US20030191059A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C3
; CURRENT APPLICATION NUMBER: US/10/223,082
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; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-223-082-15

Query Match      86.5%; Score 1468.4; DB 16; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCCAAATACACCTGGCACCAGAGTGA 288
DB 1 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCCAAATACACCTGGCACCAGAGTGA 60

QY 289 ATATGATGTCTCATAGAAGGTGAATCGGAGAGCGATGAGGAGAGCAATGTGACAAAGTA 348
DB 61 ATATGATGTCTCATAGAAGGTGAATCGGAGAGCGATGAGGAGAGCAATGTGACAAAGTA 120

QY 349 TGAGGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTGTCTGTGTGTGTGTGTGTGTGTGT 408
DB 121 TGAGGCCAGGCACTCTCAGCCAGCTGGTGCCATCACTGTCTGTGTGTGTGTGTGTGTGTGT 180

QY 409 CGGTGTCTGGCAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
DB 181 CGGTGTCTGGCAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

QY 469 CGTGGAAATATCTATCTTAAACTTGGCAGTCTTAACTGTGTGTGTGTGTGTGTGTGTGTGT 528
DB 241 CGTGGAAATATCTATCTTAAACTTGGCAGTCTTAACTGTGTGTGTGTGTGTGTGTGTGTGT 300

QY 529 GCCCTTCTGGCTCATCTGTGGGGCGATCCATGTGTAAATTTCTCATTGGACTGTACTT 588
DB 301 GCCCTTCTGGCTCATCTGTGGGGCGATCCATGTGTAAATTTCTCATTGGACTGTACTT 360

QY 589 CGTGGCCCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAGGTACCTAGT 648
DB 361 CGTGGCCCTGTACAGTGAGACATTTTCAATTGCCCTTCTGACTGTGCAAGGTACCTAGT 420

QY 649 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGAGGGGTCCCTGTGGCATCATTTAC 708
DB 421 GTTTTGTGCAAGGGCAACTTTTCTCAGCCAGAGAGGGTCCCTGTGGCATCATTTAC 480

QY 709 AAGTGTCTGGCATGGGTAAACAGCCATTTGCGCCACTTTGCGCTGAATACGTGTGTGTATAA 768
DB 481 AAGTGTCTGGCATGGGTAAACAGCCATTTGCGCCACTTTGCGCTGAATACGTGTGTGTATAA 540

QY 769 ACCTCAGATGGAAGACAGAGAAATACAAAGTGTGTGATTTAGCAGAACTCCCTTCTGCGCAG 828
DB 541 ACCTCAGATGGAAGACAGAGAAATACAAAGTGTGTGATTTAGCAGAACTCCCTTCTGCGCAG 600
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RESULT 12

US-10-305-654-15

; Sequence 15, Application US/10305654

; Publication No. US20030224984A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hans-Peter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

```
QY 829 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTTCGGTCTTGTCTCT 888
DB 601 TGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAAAATGAACATTTTCGGTCTTGTCTCT 660

QY 889 CCCCCTATTATTTTATACATTTCTATGTGCAAAATGAGAAAAACACTAAGTTTCAGGGA 948
DB 661 CCCCCTATTATTTTATACATTTCTATGTGCAAAATGAGAAAAACACTAAGTTTCAGGGA 720

QY 949 GCAGAGGTATAGCTTTTCAAGCTTGTGTTTGGCATAATGTTAGTCTTCTCTCTGTGTGTG 1008
DB 721 GCAGAGGTATAGCTTTTCAAGCTTGTGTTTGGCATAATGTTAGTCTTCTCTCTGTGTGTG 780

QY 1009 GGCGCCCTACAAATATTGCAATTTTCTGTGCCACTTTTCAAAAGAACACTTTCTCCCTGAGTGA 1068
DB 781 GGCGCCCTACAAATATTGCAATTTTCTGTGCCACTTTTCAAAAGAACACTTTCTCCCTGAGTGA 840

QY 1069 CTGCAAGAGCAGCTACAAATCTGCAAAAAGTGTTCACATCACTAAATCTATCGCCACAC 1128
DB 841 CTGCAAGAGCAGCTACAAATCTGCAAAAAGTGTTCACATCACTAAATCTATCGCCACAC 900

QY 1129 CCACTGCTGCATCAACCCCTCTCTCTGTATGCTTCTTGTATGGGACATTTTAGCAAAATACCT 1188
DB 901 CCACTGCTGCATCAACCCCTCTCTCTGTATGCTTCTTGTATGGGACATTTTAGCAAAATACCT 960

QY 1189 CTGCGCGCTGTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1248
DB 961 CTGCGCGCTGTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1020

QY 1249 AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATTCACACCAAT 1308
DB 1021 AGGCACATCGAGGGAAGAACCTGACCATTTCCACCGAAGTGTAACTAGCATTCACACCAAT 1080

QY 1309 GCAAGAAGAAATAAACAATGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC 1368
DB 1081 GCAAGAAGAAATAAACAATGATTTTTCATCTTCTGCAATTTTTCATGTAATTTTCTACAC 1140

QY 1369 ATTTGTATACAAATCGGATACAGGAAGAAAAGGAGAGGTGAGTAACTTTGCTAAGC 1428
DB 1141 ATTTGTATACAAATCGGATACAGGAAGAAAAGGAGAGGTGAGTAACTTTGCTAAGC 1200

QY 1429 ACTGAATTTGTCTCAGGCAACCGTGCAAGGTCTTTTACAAACGTGAGTCTCTTCCGCTCTCT 1488
DB 1201 ACTGAATTTGTCTCAGGCAACCGTGCAAGGTCTTTTACAAACGTGAGTCTCTTCCGCTCTCT 1260

QY 1489 ACCACTTGTCCATAGTGTGATAGGACTAGTCTCTCTCTGAGAGAAACCTAAGGCG 1548
DB 1261 ACCACTTGTCCATAGTGTGATAGGACTAGTCTCTCTCTGAGAGAAACCTAAGGCG 1320

QY 1549 CGGAATTTGTCTAAGATCACTTAAGTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGT 1608
DB 1321 CGGAATTTGTCTAAGATCACTTAAGTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGT 1380

QY 1609 AGCATTTGTCTAGAGCCTACGTTTGTGTCAGAACATCAAACTCCAAACCTCGGGGACAAA 1668
DB 1381 AGCATTTGTCTAGAGCCTACGTTTGTGTCAGAACATCAAACTCCAAACCTCGGGGACAAA 1440

QY 1669 CGACATGAATTAATGATTTTAAACATC 1698
DB 1441 CGACATGAATTAATGATTTTAAACATC 1470
```

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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 15
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-305-654-15

Query Match      86.5%; Score 1468.4; DB 17; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCCAAATTACAGCTGGGACACGAGATGA 288
DB 1 GGAGCTCAGCCAGTGGGAGTCTGAAGATGGCCAAATTACAGCTGGGACACGAGATGA 60

QY 289 ATATGATGTCCTCATAGAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAGTA 348
DB 61 ATATGATGTCCTCATAGAGGTGAATCGAGAGCGATGAGGAGAGCAATGTGACAGTA 120

QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCCTCTGCTGCTGTGTGTGTGAT 408
DB 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCCTCTGCTGCTGTGTGTGAT 180

QY 409 CGGTGTCCTGGCAATCTCCTGGTGTGCTTATCTCGGTAAATATAAAGACTCAAAAG 468
DB 181 CGGTGTCCTGGCAATCTCCTGGTGTGCTTATCTCGGTAAATATAAAGACTCAAAAG 240

QY 469 CGTGGAATATCTATCTTCTAACTGGGAGTCTTCTAATCTGCTGCTTCTGCTTACCT 528
DB 241 CGTGGAATATCTATCTTCTAACTGGGAGTCTTCTAATCTGCTGCTTCTGCTTACCT 300

QY 529 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACT 588
DB 301 GCCCTTCTGGGCTCATGCTGGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACT 360

QY 589 CGTGGCCCTGTACAGTGAGACATTTTTCATTTGCAATTTGCTGCTGCTGCAAGGTA 648
DB 361 CGTGGCCCTGTACAGTGAGACATTTTTCATTTGCAATTTGCTGCTGCTGCAAGGTA 420

QY 649 GTTTTGGACAGGGCACTTTTCTCAGCCAGGAGGAGTGCCTGTGGCATCATTTAC 708
DB 421 GTTTTGGACAGGGCACTTTTCTCAGCCAGGAGGAGTGCCTGTGGCATCATTTAC 480

QY 709 AAGTGTCTGGCATGGGTAAACGCCATTTCTGGCCACTTTTGGCTGTAATAGCTGTTTATAA 768
DB 481 AAGTGTCTGGCATGGGTAAACGCCATTTCTGGCCACTTTTGGCTGTAATAGCTGTTTATAA 540

QY 769 ACTCAGATGGAAGACAGAAATATAAGTGTGCAATTTAGAGAACTCCCTTCTGCGCAGC 828
DB 541 ACTCAGATGGAAGACAGAAATATAAGTGTGCAATTTAGAGAACTCCCTTCTGCGCAGC 600

QY 829 TGATGAGACATTTCTGGAAGCATTTCTGACTTTTAAATGAACATTTCTGCTTCTGCT 888
DB 601 TGATGAGACATTTCTGGAAGCATTTCTGACTTTTAAATGAACATTTCTGCTTCTGCT 660

QY 889 CCCCTTATTTTATTTTACATTTCTCTATGTGCAATTTAGAGAAATGAGAGAAATCAAGGTT 948
DB 661 CCCCTTATTTTATTTTACATTTCTCTATGTGCAATTTAGAGAAATGAGAGAAATCAAGGTT 720
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QY 949 GCAGAGGTATAGCCTTTTCAAGCTTGTTTTGGCCATAATGGTAGTCTTCTTCTGATGG 1008
DB 721 GCAGAGGTATAGCCTTTTCAAGCTTGTTTTGGCCATAATGGTAGTCTTCTTCTGATGG 780

QY 1009 GGGGCCCTTACAAATATTGCAATTTTCTGTCCACTTTTCAAGAAACACTTCTCCCTGAGTGA 1068
DB 781 GGGGCCCTTACAAATATTGCAATTTTCTGTCCACTTTTCAAGAAACACTTCTCCCTGAGTGA 840

QY 1069 CTGCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACATCATCTAAACTCATCGCCACCAC 1128
DB 841 CTGCAAGAGCAGCTACAAATCTGGACAAAGTGTTCACATCATCTAAACTCATCGCCACCAC 900

QY 1129 CCATGCTGTCATCAACCTCTCCTGTATGCGTTCCTTGTGATGGACATTTAGCAATACCT 1188
DB 901 CCATGCTGTCATCAACCTCTCCTGTATGCGTTCCTTGTGATGGACATTTAGCAATACCT 960

QY 1189 CTGCGCTGTTTCCATCTCGGTAGTAACAACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1248
DB 961 CTGCGCTGTTTCCATCTCGGTAGTAACAACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1020

QY 1249 AGGCATCTGAGGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACAAAT 1308
DB 1021 AGGCATCTGAGGGGAAGAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCACAAAT 1080

QY 1309 GCAAGAAGATTAACATGGATTTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1368
DB 1081 GCAAGAAGATTAACATGGATTTTTCATCTTTCTGCAATTTTTCATGTAATTTTCTACAC 1140

QY 1369 ATTTGTATACAAATCTCGGATACAGGAAGAAAGGAGAGGTGAGCTAACATTTGCTAAGC 1428
DB 1141 ATTTGTATACAAATCTCGGATACAGGAAGAAAGGAGAGGTGAGCTAACATTTGCTAAGC 1200

QY 1429 ACTGAATTTGCTCAGGCAACCGTCAAGGCTTTTCAAAACGTGAGCTCTTTCGCTCTCT 1488
DB 1201 ACTGAATTTGCTCAGGCAACCGTCAAGGCTTTTCAAAACGTGAGCTCTTTCGCTCTCT 1260

QY 1489 ACCACTTGTCCATAGTGTGGATAGACTAGTCTCATTTCTCTGAGAGAAACTAAGGCG 1548
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QY 1549 CGGAAATTTGCTTAAGATCACCTTAACCTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGT 1608
DB 1321 CGGAAATTTGCTTAAGATCACATACTAGGAAGTGGCAGAACTGATTTCTCCAGCCCTGT 1380

QY 1609 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACTCAAACTCCAAAACCTCGGGGACAAA 1668
DB 1381 AGCATTTGCTCAGAGCCTACGCTTGGTCCAGAACTCAAACTCCAAAACCTCGGGGACAAA 1440

QY 1669 CGACATGAATTAATGTATTTTAAACATC 1698
DB 1441 CGACATGAATTAATGTATTTTAAACATC 1470
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RESULT 13
US-10-081-056-15
; Sequence 15, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
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APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574

PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
LENGTH: 1475
TYPE: DNA
ORGANISM: Homosapiens
US-10-081-056-15

Query Match 86.5%; Score 1468.4; DB 18; Length 1475;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1469; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 229 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA 288
DB 1 GGAGCTCAGCCAGTGGGCGAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA 60
QY 289 ATATGATGTCCTCATAGAAGTGAACTGGAGAGCGATGAGGAGAGCAATGTGCAAGTA 348
DB 61 ATATGATGTCCTCATAGAAGTGAACTGGAGAGCGATGAGGAGAGCAATGTGCAAGTA 120
QY 349 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCCTCTGCTCTGCTGTGTTGTGAT 408
DB 121 TGACGCCAGGCACTCTCAGCCAGCTGGTGCCATCCTCTGCTCTGCTGTGTTGTGAT 180
QY 409 CGGTGTCCTGGCAATCTCCTGTTGCTTATCTCTGTTAAATATAAAGGACTCAAAACG 468
DB 181 CGGTGTCCTGGCAATCTCCTGTTGCTTATCTCTGTTAAATATAAAGGACTCAAAACG 240
QY 469 CGTGGAAAATATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCC 528
DB 241 CGTGGAAAATATCTATCTTTCTAAACTTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCC 300
QY 529 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTGTAATAATCTCATTTGGACTGTACTT 588
DB 301 GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTGTGTAATAATCTCATTTGGACTGTACTT 360
QY 589 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCCCTTCTGACTGTGCAAGGTGACCTAGT 648
DB 361 CGTGGGCTGTACAGTGAGACATTTTCAATTTGCCCTTCTGACTGTGCAAGGTGACCTAGT 420
QY 649 GTTTTGGCAAGGGCAACTTTTTCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTAC 708
DB 421 GTTTTGGCAAGGGCAACTTTTTCTCAGCCAGGAGGGGTGCCCTGTGGCATCATTTAC 480
QY 709 AAGTGTCTGGCATGGGTAACAGCCATTTCTGGCCACTTTGGCCCTGAATAGCTGTTTATAA 768
DB 481 AAGTGTCTGGCATGGGTAACAGCCATTTCTGGCCACTTTGGCCCTGAATAGCTGTTTATAA 540
QY 769 ACCTCAGATGGGAAGACCAAGATACAAAGTGTGCAATTTAGCAGAACTTCTTCTGCGCAGC 828
DB 541 ACCTCAGATGGGAAGACCAAGATACAAAGTGTGCAATTTAGCAGAACTTCTTCTGCGCAGC 600
QY 829 TGATGAGACATTTCTGGAAGCACTTTTCTGACTTTTAAAAATGAAACATTTCTGTTCTCT 888
DB 601 TGATGAGACATTTCTGGAAGCACTTTTCTGACTTTTAAAAATGAAACATTTCTGTTCTCT 660
QY 889 CCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAAAACAATAGGTTTCAGGGA 948
DB 661 CCCCTATTTTATTTTACATTTCTCTATGTGCAATGAGAAAAACAATAGGTTTCAGGGA 720
QY 949 GCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCCATATGTTAGTCTTCTTCTGATG 1008
DB 721 GCAGAGGTATAGCCCTTTTCAAGCTTGTGTTTGGCCATATGTTAGTCTTCTTCTGATG 780
QY 1009 GCGGCCCTACAAATATTTGCAATTTTCTGTCCACTTTTCAAGAACACACTTCTTCTCCTGAGTGA 1068

Db 781 GGGGCGCTACATATATGCAATTTTCTGTGCACTTTCAAGAAACACTTCTCCCTGAGTGA 840
Qy 1069 GTGCAAGAGCAGCTCAATCTCGGACAAAAGTGTTCACATCACTAAACATCATCGCCACCAC 1128
Db 841 CTGCAAGAGCAGCTCAATCTCGGACAAAAGTGTTCACATCACTAAACATCATCGCCACCAC 900
Qy 1129 CCACCTGCTGCATCAACCCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATCCT 1188
Db 901 CCACCTGCTGCATCAACCCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATCCT 960
Qy 1189 CTGCGCGCTGTTTCCATCTCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1248
Db 961 CTGCGCGCTGTTTCCATCTCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACA 1020
Qy 1249 AGGCACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCACCAAT 1308
Db 1021 AGGCACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCACCAAT 1080
Qy 1309 GCAAGNAGNATAAATGCAATGCAATTTTCTCTTCTGCAATTTTCTGATGTAATTTTCTACAC 1368
Db 1081 GCAAGNAGNATAAATGCAATGCAATTTTCTCTTCTGCAATTTTCTGATGTAATTTTCTACAC 1140
Qy 1369 ATTTGTATACAAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAAATTTGCTAAGC 1428
Db 1141 ATTTGTATACAAAATCGGATACAGGAAGAAAGGAGAGGTGAGCTAAATTTGCTAAGC 1200
Qy 1429 ACTGAATTTGCTCAGGCAACCGTCAAGGCTCTTTTCAAAAGTGAAGTCTCTTCGCTCCT 1488
Db 1201 ACTGAATTTGCTCAGGCAACCGTCAAGGCTCTTTTCAAAAGTGAAGTCTCTTCGCTCCT 1260
Qy 1489 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCGAAGTGTAACTAAGGG 1548
Db 1261 ACCACTTGTCCATAGTGTGGATAGGACTAGTCTCATTTCTCGAAGTGTAACTAAGGG 1320
Qy 1549 CGGAAATTTGCTAAGATCACTTAAGTGAAGTGGCAGAACTGATTTCTCCAGCCCTGCT 1608
Db 1321 CGGAAATTTGCTAAGATCACTTAAGTGAAGTGGCAGAACTGATTTCTCCAGCCCTGCT 1380
Qy 1609 AGCATTTGCTCAGAGCTTACGTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1668
Db 1381 AGCATTTGCTCAGAGCTTACGTTGGTCCAGAACATCAAACTCCAAACCTCGGGACAAA 1440
Qy 1669 CGCATGAATGAATGAATTTTAAACATC 1698
Db 1441 CGCATGAATGAATGAATTTTAAACATC 1470

RESULT 14
US-10-225-567A-353
; Sequence 353, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 353
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-353

Query Match 85.7%; Score 1455.2; DB 15; Length 1645;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 239 CCAGTGGGCGAGTCTGAAGATGGCCCAATTTACAGCTGGCACCCAGAGGATGAATATATGTC 298
Db 185 CCACAGGCGAGTCTGAAGATGGCCCAATTTACAGCTGGCACCCAGAGGATGAATATATGTC 244
Qy 239 CTCATAGAAGGTGAACCTGGAGAGCGATGAGCGACAGCAATGTGACAAAGTATGACGCCCCAG 358
Db 245 CTCATAGAAGGTGAACCTGGAGAGCGATGAGCGAGCAATGTGACAAAGTATGACGCCCCAG 304
Qy 359 GCACCTCTCAGCCCGAGCTGGTCCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTG 418
Db 305 GCACCTCTCAGCCCGAGCTGGTCCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTCTCTG 364
Qy 419 GACAAATCTCTGTTGTTGCTTATCTCTGTTAAATATAAAGGACTCAAAACGCGTGAATAAT 478
Db 365 GACAAATCTCTGTTGTTGCTTATCTCTGTTAAATATAAAGGACTCAAAACGCGTGAATAAT 424
Qy 479 ATCTATCTCTTAAACTTGGCAGTTTCTAACTGTGTGTTTCTTGTCTTACCTGCCCCTCTGG 538
Db 425 ATCTATCTCTTAAACTTGGCAGTTTCTAACTGTGTGTTTCTTGTCTTACCTGCCCCTCTGG 484
Qy 539 GCTCATGCTGGGGCGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGGCTG 598
Db 485 GCTCATGCTGGGGCGATCCCATGTGTAAAAATTTCTCATTTGGACTGTACTTCTGTGGGCTG 544
Qy 599 TACAGTGAGACATTTTCAATTTGCCCTTCTGACTGTGCAAGGACTAGTGTGTTTTCAC 658
Db 545 TACAGTGAGACATTTTCAATTTGCCCTTCTGACTGTGCAAGGACTAGTGTGTTTTCAC 604
Qy 659 AAGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGCACTCATTTACAAAGTGTCTG 718
Db 605 AAGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGCACTCATTTACAAAGTGTCTG 664
Qy 719 GCATGGGTAAACAGCCATTTCTGGCCCACTTTGCTGCTGAATACGTGGTTTATAAACCTCAGATG 778
Db 665 GCATGGGTAAACAGCCATTTCTGGCCCACTTTGCTGCTGAATACGTGGTTTATAAACCTCAGATG 724
Qy 779 GAAGCCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACA 838
Db 725 GAAGCCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAGACA 784
Qy 839 TTCTGGAAGCAATTTTCTGACTTTAAATGAACATTTTCGGTTCTTGTCTCTCCCTCATTT 898
Db 785 TTCTGGAAGCAATTTTCTGACTTTAAATGAACATTTTCGGTTCTTGTCTCTCCCTCATTT 844
Qy 899 ATTTTACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGGTAT 958
Db 845 ATTTTACATTTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGGTAT 904
Qy 959 AGCCTTTTCAAGCTGTTTTTGGCCATATATGTTAGTCTTCTCTCTGATGTGGGCGCCCTAC 1018
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Qy 1019 AATATTGCAATTTTCTCTGCTCCACTTTCAAGAAACACTTCTCCCTGAGTGACTGCAAGAGC 1078
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Qy 1139 ATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCGCTG 1198
Db 1085 ATCAACCCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAAATACCTCTGCGCGCTG 1144
Qy 1199 TTCCATCTGCTGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCAATCG 1258
Db 1145 TTCCATCTGCTGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCAATCG 1204
Qy 1259 AGGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAATGCAAGAGAA 1318
Db 1205 AGGGAAGAACCTGACCAATTCACCGAAGTGTAAACTAGCATCCACCAATGCAAGAGAA 1264

Qy	1559	TCTAAGATC	ACTTA	ACTAGG	AAGTGG	CAGAACT	GATTTCT	CCAGCCCT	GGTAGCAT	TTGCT	1618
Db	97944	TCTAAGAT	CACATA	AACTAG	GAAGTGG	CAGAACT	GATTTCT	CCAGCCCT	GGTAGCAT	TTGCT	98003
Qy	1619	CAGAGCCT	ACGCTT	GGTCC	AGACAT	CCAACT	CCAAAC	CTGGG	GACAAAC	GACATG	1678
Db	98004	CAGAGCCT	ACGCTT	GGTCC	AGACAT	CCAACT	CCAAAC	CTGGG	GACAAAC	GACATG	98063
Qy	1679	TAAATGT	ATTTT	TAA	AACATC						1698
Db	98064	TAAATGT	ATTTT	TAA	AACATC						98083

Search completed: June 18, 2005, 20:05:12
Job time : 1076 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:34:54 ; Search time 666.776 Seconds
(without alignments)
9615.040 Million cell updates/sec

Title: US-10-623-472-32

Perfect score: 1083

Sequence: 1 atggataactacacagtggc.....aaaggcaggataataataa 1083

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1083	100.0	1083	6	ABSS2093 Mouse CCR
2	1076.6	99.4	1083	12	Ado30354 Mouse GPC
3	1076.6	99.4	2045	6	Aad32931 Mus muscu
4	423.2	39.1	1646	13	Adq38349 Human SNP
5	423.2	39.1	1776	13	Adq38350 Human SNP
6	422	39.0	1140	12	ACH89585 Human gen
7	422	39.0	1475	6	ABL88079 Human pro
8	422	39.0	1475	6	ABL95568 Human ang
9	422	39.0	1475	10	ADD10304 Human sec
10	422	39.0	1475	10	ADD11264 Human sec
11	422	39.0	1475	10	ADD37057 Human sec
12	422	39.0	1475	12	ADH41265 Human sec
13	422	39.0	1475	12	ADH43448 Human PRO
14	422	39.0	1475	12	ADK82793 Human PRO
15	422	39.0	1645	8	ABZ42782 Human che
16	422	39.0	1645	11	ADN95729 Human BEC
17	422	39.0	1645	13	ADP24442 PRO polyp
18	422	39.0	1645	13	ADST75309 Human CCR
19	422	39.0	1698	12	ADP13564 Renal cel
20	422	39.0	143040	11	ABD20648 Human pul

21	422	39.0	143067	11	ABD20815	Human pul
22	422	39.0	143068	3	AAA34983	Human ade
23	422	39.0	143068	3	AAA35150	Human ade
24	422	39.0	143068	3	AAF21272	Human low
25	422	39.0	143068	3	AAF21105	Human low
26	422	39.0	143068	6	ABL68124	Ovary can
27	422	39.0	143068	6	ABT11034	Human bre
28	422	39.0	143068	10	ABZ96966	Human nuc
29	422	39.0	143068	10	ABZ96799	Human nuc
30	422	39.0	149412	3	AAA35151	Human ade
31	422	39.0	152739	11	ABD20816	Human pul
32	422	39.0	152740	3	AAF21273	Human low
33	422	39.0	152740	10	ABZ96967	Human nuc
34	421.6	38.9	1270	10	ACA56158	Human sig
35	421.6	38.9	1270	12	ADI55954	Human pol
36	421.2	38.9	1316	2	AAT99543	Human che
37	420.4	38.8	1547	2	AAV15419	Human mac
38	420.4	38.8	1547	10	ABX95937	Human mon
39	420.4	38.8	1547	12	ADQ67844	Human CDN
40	412.4	38.1	1035	6	ABSS2092	Human CCR
41	412.4	38.1	1035	12	ADQ30063	Human GPC
42	412	38.0	1251	11	ADP03560	Human GPC
43	398.4	36.8	1050	2	AAV04641	cDNA enco
44	398.4	36.8	1050	6	AAAS17436	Human CDN
45	398.4	36.8	1050	6	AAD42836	Human G-p

ALIGNMENTS

RESULT 1

ABSS2093

ID ABSS2093 standard; cDNA; 1083 BP.

AC ABSS2093;

XX 05-NOV-2002 (first entry)

DT Mouse CCR12 cDNA.

DE Mouse CCR12 cDNA.

XX Mouse; CCR12; gene; ss; chemokine receptor; L-CCR; MCP-1; HBK cell;

KW Monocyte Chemoattractant Protein-1; brain glial cell; ischaemia; asthma;

KW inflammatory disease; degenerative brain disease; Alzheimer's disease;

KW multiple sclerosis; neurodegenerative disease; neuroinflammatory disease;

KW allergic encephalitis; chronic obstructive pulmonary disease;

KW obstructive airway disease; neuroprotective; antiinflammatory.

XX Mus sp.

OS Mus sp.

XX WO200257779-A2.

PN 25-JUL-2002.

PD 18-JAN-2002; 2002WO-NL000039.

XX 18-JAN-2001; 2001EP-00200181.

PR (UYGR-) RIJKSUNIV GRONINGEN.

XX Boddeke EHWGM, Biber K;

PI WPI; 2002-599725/64.

DR Identifying compounds for treating inflammatory or degenerative brain

XX diseases, comprises testing the compound for its capacity to modulate or

PT mimic Monocyte Chemoattractant Protein-1 binding with a chemokine

XX receptor.

PS Disclosure; Fig 8; 45pp; English.

XX The invention relates to identifying a candidate drug compound comprising

CC testing the compound for its capacity to modulate or mimic Monocyte

CC Chemoattractant Protein-1 (MCP-1) binding with a chemokine receptor

CC capable of being expressed on brain glial cells and is known in the mouse
CC as L-CCR or in humans as CRAW-B. The chemokine receptor expressed in a
CC cultured cell comprising the cell transfected with a nucleic acid and a
CC HEK cell, is useful in identifying a candidate drug compound for treating
CC inflammatory or degenerative brain disease, e.g. ischaemia, Alzheimer's
CC disease or multiple sclerosis. The agonist or antagonist is useful in the
CC preparation of the pharmaceutical composition useful in treating
CC neurodegenerative and neuroinflammatory diseases such as allergic
CC encephalitis and chronic obstructive pulmonary disease and obstructive
CC airway diseases such as asthma. This sequence represents mouse L-CCR
CC cDNA, also known as CCR12
XX
SQ

Sequence 1083 BP; 237 A; 294 C; 274 G; 278 T; 0 U; 0 Other;

Query Match 100.0%; Score 1083; DB 6; Length 1083;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGATAACTACACAGTGGCCCGGACGATGATATGATCTCTAATCTTAGACGACTAC	60
Db	1	ATGGATAACTACACAGTGGCCCGGACGATGATATGATCTCTAATCTTAGACGACTAC	60
Qy	61	CTGGACAACAGTGGCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCAGCAGGTG	120
Db	61	CTGGACAACAGTGGCGGACCAAGTTCCGCGCCCGGAGTTCTCTCCCGCCAGCAGGTG	120
Qy	121	CTGCAGTTCTGCTGCGCGGTGTTTGGCGTGGTCTCTTGGACAACGTCGTGGCGGTGTTT	180
Db	121	CTGCAGTTCTGCTGCGCGGTGTTTGGCGTGGTCTCTTGGACAACGTCGTGGCGGTGTTT	180
Qy	181	ATCTTGTTGAAATACAAAGACATCAAGATCTGGGAACATCTACTTCTTAAACCTGGCA	240
Db	181	ATCTTGTTGAAATACAAAGACATCAAGATCTGGGAACATCTACTTCTTAAACCTGGCA	240
Qy	241	CTTTCAAACCTGTGTTTCTCGCTTCCCTCGGTTCTGGGCCCATCTATCGACACACGGG	300
Db	241	CTTTCAAACCTGTGTTTCTCGCTTCCCTCGGTTCTGGGCCCATCTATCGACACACGGG	300
Qy	301	GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCACCTCTGGGCTTATAC	360
Db	301	GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCACCTCTGGGCTTATAC	360
Qy	361	AGGAGGTGTTTTCACACATCTCTCTCTGTGCAAGATACAGGGTGTTCCTCCAGGG	420
Db	361	AGGAGGTGTTTTCACACATCTCTCTCTGTGCAAGATACAGGGTGTTCCTCCAGGG	420
Qy	421	CGACTGGCCCTCCATCTTTCACGACAGTGTCTTGTGGTATTTGCTGTCATCTCTGGCATGG	480
Db	421	CGACTGGCCCTCCATCTTTCACGACAGTGTCTTGTGGTATTTGCTGTCATCTCTGGCATGG	480
Qy	481	GCCATGGCTACTGGGCTCTCTTTGGCCGAGTCTGTGTTTATGAGCCTCGGATGGAAGA	540
Db	481	GCCATGGCTACTGGGCTCTCTTTGGCCGAGTCTGTGTTTATGAGCCTCGGATGGAAGA	540
Qy	541	CAGAAACACAAAGTGTGCTTTGGCAACCTCACCTTCTTGCAATCGAAGCGCGCTCTGG	600
Db	541	CAGAAACACAAAGTGTGCTTTGGCAACCTCACCTTCTTGCAATCGAAGCGCGCTCTGG	600
Qy	601	AAGTACGTTCTGACGTCACAAATGATCATCTGCTACTTCTCTCTCTGCTGTTT	660
Db	601	AAGTACGTTCTGACGTCACAAATGATCATCTGCTACTTCTCTCTCTGCTGTTT	660
Qy	661	ATAATCTGCTGCAGGCAACTGAGGAGAGGAGGCTTCAGGGAGAGACAGTACGACCTC	720
Db	661	ATAATCTGCTGCAGGCAACTGAGGAGAGGAGGCTTCAGGGAGAGACAGTACGACCTC	720
Qy	721	CACAAGCGGCTCTGTGTATAACGGGCTGTCTCTTTGATGTGGGGCTCTTACCAACT	780
Db	721	CACAAGCGGCTCTGTGTATAACGGGCTGTCTCTTTGATGTGGGGCTCTTACCAACT	780
Qy	781	GTGCTTTTCTGCTGCTTTCCAGGAACACTTGTCTCTGAGGATGAGAGAGAGCTAC	840
Db	781	GTGCTTTTCTGCTGCTTTCCAGGAACACTTGTCTCTGAGGATGAGAGAGAGCTAC	840

Qy	841	CACCTGGACGCAAGTGTTCAGGTCAACAGCTGGTAGCGACACCCACTGCTGCTCAAC	900
Db	841	CACCTGGACGCAAGTGTTCAGGTCAACAGCTGGTAGCGACACCCACTGCTGCTCAAC	900
Qy	901	CGCTGCTCTTATTTGCTTCTTGACCGGAAGGCTTTATGAGATACCTTCGACGCTGTTT	960
Db	901	CGCTGCTCTTATTTGCTTCTTGACCGGAAGGCTTTATGAGATACCTTCGACGCTGTTT	960
Qy	961	CCACGGTCAATGATATCCCTTATCCCTTATCAAGTAGTGGAGGCTATCAGCAAGCGCTCCAAG	1020
Db	961	CCACGGTCAATGATATCCCTTATCCCTTATCAAGTAGTGGAGGCTATCAGCAAGCGCTCCAAG	1020
Qy	1021	GRAGTCTATGGCAGGCGCCATTTGAACCTGACAGCAATTTGCATCAAGGCGAGGATATAATA	1080
Db	1021	GRAGTCTATGGCAGGCGCCATTTGAACCTGACAGCAATTTGCATCAAGGCGAGGATATAATA	1080
Qy	1081	TAA 1083	
Db	1081	TAA 1083	

RESULT 2
ADO30354

ID ADO30354 standard; cDNA; 1083 BP.

AC ADO30354;

XX 29-JUL-2004 (first entry)

XX Mouse GPCR CMKBR1L2 polynucleotide, SEQ ID NO:1457.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX colon disorder; intestinal disorder; cardiovascular disorder;
XX muscular disorder; blood disorder; immune disorder; bone disorder;
XX joint disorder; metabolic disorder; nutritive disorder; cancer;
XX kidney disorder; liver disorder; lung disorder; breast disorder;
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
XX cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
XX virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
XX dermatological; antiulcer; antihypertensive; antiallergic; anorectic;
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
XX murine; gene; ss.

XX Mus musculus.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX P-PSDB; ADO29712.

XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1457; 542pp; English.

Db	1525 TAA 1527	Best Local Similarity 65.2%; Pred. No. 5.8e-117; Matches 706; Conservative 5; Mismatches 338; Indels 33; Gaps 5;
RESULT 4		
ADQ38349		
ID	ADQ38349 standard; DNA; 1646 BP.	
XX		
AC	ADQ38349;	
XX		
DT	18-NOV-2004 (first entry)	
XX		
DE	Human SNP containing myocardial infarction-associated gene, SEQ ID 12.	
XX		
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;	
KW	cardiac; gene therapy; human; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
FN	WO2004058052-A2.	
PD	15-JUL-2004.	
XX		
PF	22-DEC-2003; 2003WO-US040978.	
XX		
PR	20-DEC-2002; 2002US-0434778P.	
PR	10-MAR-2003; 2003US-0453135P.	
PR	30-APR-2003; 2003US-0466412P.	
PR	23-SEP-2003; 2003US-0504955P.	
XX		
PA	(APPL-) APPLERA CORP.	
XX		
PI	Cargill M, Devlin JJ, Iakoubova O;	
XX		
DR	WPI; 2004-533949/51.	
DR	P-PSDB; ADQ383177.	
XX		
PT	Identifying an individual who has an altered risk for developing	
PT	myocardial infarction by detecting a single nucleotide polymorphism in	
PT	the individual's nucleic acids.	
XX		
PS	Claim 7; SEQ ID NO 12; 145pp; English.	
XX		
CC	The invention relates to a novel method for identifying an individual who	
CC	has an altered risk for developing myocardial infarction. The method	
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of	
CC	the nucleotide sequences given in the specification in the individual's	
CC	nucleic acids, where the presence of the SNP is correlated with an	
CC	altered risk for myocardial infarction in the individual. The invention	
CC	further comprises: an isolated nucleic acid molecule comprising at least	
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in	
CC	the specification or its complement and encoding any one of the amino	
CC	acid sequences given in the specification; an isolated polypeptide	
CC	comprising an amino acid sequence given in the specification; an antibody	
CC	that specifically binds to the polypeptide or its antigen-binding	
CC	fragment; an amplified polynucleotide containing an SNP given in the	
CC	specification and which is between about 16 and 1000 nucleotides in	
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the	
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a	
CC	nucleic acid molecule; a method of detecting a variant polypeptide; and a	
CC	method for identifying an agent useful in treating or preventing	
CC	myocardial infarction. The novel detection method has cardiac activity.	
CC	The nucleic acids of the invention may be used in gene therapy. The	
CC	method is useful in identifying an individual who has an increased or	
CC	decreased risk for developing myocardial infarction and for preparing a	
CC	composition for treating or preventing myocardial infarction. This	
CC	polynucleotide sequence represents a human myocardial infarction-	
CC	associated gene containing one or more SNP's of the invention. Note: This	
CC	sequence was not shown in the specification. The sequence has come from	
CC	an electronic sequence listing downloaded from the WIPO website.	
XX		
SQ	Sequence 1646 BP; 438 A; 381 C; 356 G; 459 T; 0 U; 12 Other;	
	Query Match 39.1%; Score 423.2; DB 13; Length 1646;	

Qy	1	ATGGATTAACACAGTGGCCCGACGATGAATATGATGTCCTTAATCTTAGACGACTAC	60
Db	202	ATGGCCAATTRCAGCTGGCCACGAGGATGAATATGATGTCCTTAATCTTAGACGACTAC	258
Qy	61	CTGGACAACAGTGGCCCGGACCAAGTT-----CCGGCCCCCGAGTTCTCTCCCCCAG	114
Db	259	CTGGAGAGCGATGAGGCGAGCAATGTGACAAGATGACGCCAGGCACTCTCAGCCAG	318
Qy	115	CAGTGTGCGAGTCTGCTGCGCGGTTCGGGTGGTCTCTTGGACAACAGTGTGGCG	174
Db	319	CTGGTGCACACTCTGCTCTGCTGTGTTGTGATCGGTGCTCTGGACAATCTCTCGTT	378
Qy	175	GTGTTTATCTTGGTGAATACAAAGGACTCAAGAATCTGGGGAAACATCTACTTCTTAAC	234
Db	379	GTGCTTATCTCGTAAATATATAAGGACTCAACCGGTGGAAATATCTATCTTCTTAAC	438
Qy	235	CTGGCACTTTCAAACTGTGTTCTCTCCCTGCGCTTCTGGGCCCATATCTCAGCA	294
Db	439	TGGCAGTTTCTAACTTGTGTTCTTGTCTTACCTGCGCTTCTGGGCTCATGCTG----	493
Qy	295	CACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTGGACTCACTCTCGGGC	354
Db	494	-----RKGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGGGC	540
Qy	355	TTATACAGCGAGTGTGTTTCCCAACATCTCTCTGTGGCAAGGATACAGGGTGTTC	414
Db	541	CTGTACAGTGAGACATTTTCAATGTCCTTCTGACTGTGCAAGGATCCTAGTGTGTTG	600
Qy	415	CAAGGGCGAC---TGGCCTCCATCTTCACGACAGTGTCTGTGTGTTATTTGTCGTCATC	471
Db	601	CACAAGGGMAACTTTTCTCAGCCAGGAGGGTGCCTCTGTGCATCATTTACAGTGTG	660
Qy	472	CTGCGATGGCCATGGCTACTGCGCTCTCTTTGCGGAGTCTGTGTTTTATGAGCTCG	531
Db	661	CTGCGATGGGTAAACAGCCATTTCTGGCCACTTTGCGCTGAATWCRTGGTTTATAAAC	720
Qy	532	ATGGAAGACAGAAACAAAGTGTGCTTTGGCAAACTCACTTCTTCCCAATCGAAGCG	591
Db	721	ATGGAAGACAGAAATACAGTGTGCAATTTAGCAGAACTCCCTCTCCAGCTGATGAG	780
Qy	592	CCGCTCTGGAAGTACGTTCTGACGCTCAAAATGATCATCTTGTGTACTTTCTCTCTG	651
Db	781	ACATTTCTGGAAGCATTTTCTGACTTTAAATGAACATTTTCGGTTCTTCTCTCCCTA	840
Qy	652	CTGTTTTTATATCTCTGCGGCAACTGAGGAGAGGAGAGCTTCAGGAGAGACAG	711
Db	841	TTTATTTTATCATTTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGAGAGAGG	900
Qy	712	TACGACCTCCACAGCGGCTTTGTCTAATACGGCGTGTCTCTTTGATGTGGCGCT	771
Db	901	TATAGCTTTTCAAGCTGTTTTTGGCCCTATGTTAGTGTCTCTCTGATGTGGCGGCC	960
Qy	772	TACAACACTGTGCTTTTCTGCTGCTTTCAGGAACACTTGTCTCTCGAGGATGAGAAG	831
Db	961	TACAATATGCAATTTTCTGCTGCTTTCAGGAACACTTCTCTCTGAGTGTGCAAG	1020
Qy	832	AGAGCTACACCTCTGAGCGCAAGTGTTCAGGTTCACAGCTGTGAGGACCACTCTGC	891
Db	1021	AGCAGCTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACCACTGC	1080
Qy	892	TGCGTCAACCGCTCTATTTGCTTCTTGGCCGGAAGGCTTTTATGAGATACCTTCGC	951
Db	1081	TGCATCAACCTCTCTCTGATGCGTTTCTTGTATGGGA---CATTTAGCAATATCTCTGC	1137
Qy	952	AGCTGTTTCCACCGGTGCAATGATATCCCTCTATCAAAAGTGTGAGGCTATCAGCAAGC	1011
Db	1138	CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGC	1197
Qy	1012	CTTCAAGGAGGTCAATGGCAGGCCCATTTGAACTGTACAGCAATTTGCATCAAGGAGC	1071

Db	1198	ACATCGAGGGGAAGAACTGACCATTCACCGAAGTGTAAACTAGCATCCACAAATGCCAA	1257
Qy	1072	GA 1073	
Db	1258	GA 1259	
RESULT 5			
ADQ38350			
ID	ADQ38350	standard; DNA; 1776 BP.	
AC			
XX	ADQ38350;		
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE	Human SNP containing myocardial infarction-associated gene, SEQ ID 13.		
XX			
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;		
KW	cardiant; gene therapy; human; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004058052-A2.		
XX			
PD	15-JUL-2004.		
XX			
PF	22-DEC-2003; 2003WO-US040978.		
XX			
PR	20-DEC-2002; 2002US-0434778P.		
PR	10-MAR-2003; 2003US-0453135P.		
PR	30-APR-2003; 2003US-0466412P.		
PR	23-SEP-2003; 2003US-0504955P.		
XX			
PA	(APPL-) APPLERA CORP.		
XX			
PI	Cargill M, Devlin JJ, Iakoubova O;		
XX			
DR	WPI; 2004-533949/51.		
DR	P-PSDB; ADQ39178.		
XX			
PT	Identifying an individual who has an altered risk for developing		
PT	myocardial infarction by detecting a single nucleotide polymorphism in		
PT	the individual's nucleic acids.		
XX			
PS	Claim 7; SEQ ID NO 13; 145pp; English.		
XX			
CC	The invention relates to a novel method for identifying an individual who		
CC	has an altered risk for developing myocardial infarction. The method		
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of		
CC	the nucleotide sequences given in the specification in the individual's		
CC	nucleic acids, where the presence of the SNP is correlated with an		
CC	altered risk for myocardial infarction in the individual. The invention		
CC	further comprises: an isolated nucleic acid molecule comprising at least		
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in		
CC	the specification or its complement and encoding any one of the amino		
CC	acid sequences given in the specification; an isolated polypeptide		
CC	comprising an amino acid sequence given in the specification; an antibody		
CC	that specifically binds to the polypeptide or its antigen-binding		
CC	fragment; an amplified polynucleotide containing an SNP given in the		
CC	specification and which is between about 16 and 1000 nucleotides in		
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the		
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a		
CC	nucleic acid molecule; a method of detecting a variant polypeptide; and a		
CC	method for identifying an agent useful in treating or preventing		
CC	myocardial infarction. The novel detection method has cardiac activity.		
CC	The nucleic acids of the invention may be used in gene therapy. The		
CC	method is useful in identifying an individual who has an increased or		
CC	decreased risk for developing myocardial infarction and for preparing a		
CC	composition for treating or preventing myocardial infarction. This		
CC	polynucleotide sequence represents a human myocardial infarction-		
CC	associated gene containing one or more SNP's of the invention. Note: This		
CC	sequence was not shown in the specification. The sequence has come from		
CC	an electronic sequence listing downloaded from the WIPO website.		

Db 1264 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAAGGC 1323
 Qy 1012 CCTCAGGGGAGGTCATGGCAGGCCCATTTGAACGTATACAGCAATTTTCATCAAGGCAG 1071
 Db 1324 ACATCGAGGGAAGAACCTGACCATTCACCCAGGAGTGTAACTAGCATCCACCAATGCAA 1383
 Qy 1072 GA 1073
 Db 1384 GA 1385

RESULT 6

ACH89585
 ID ACH89585 standard; DNA; 1140 BP.

XX ACH89585;
 XX
 DT 29-JUL-2004 (first entry)
 XX Human genome derived single exon probe #22780.
 XX Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 KW
 XX Homo sapiens.
 XX
 XX US2003194704-A1.
 XX
 XX 16-OCT-2003.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX (PENNY/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 DR WPI; 2004-119264/12.
 XX

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

XX Claim 1; SEQ ID NO 22780; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX

SQ Sequence 1140 BP; 294 A; 275 C; 241 G; 330 T; 0 U; 0 Other;

Query Match 39.0%; Score 422; DB 12; Length 1140;

Best Local Similarity 65.5%; Pred. No. 1.1e-116;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGATAAATACTACACAGTGGCCCCCGGACGATGAATATATGATGTCCTTAATCTTAGACGACTAC 60
 Db 13 ATGGCCAATTTACACGCTGGCACCAGAGGATGAATATGATGTCC--TCATAGAAGGTGAA 69
 Qy 61 CTGGACAACAGTGGCCCGGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCAG 114
 Db 70 CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGCCAG 129
 Qy 115 CAGGTGCTGCAGTTCCTGCGCGGTGTTTGGGTGGTCTCTTGGACAAGCTGCTGGCG 174
 Db 130 CTGGTGCATCACTCTGCTCTGCTGTTGTGATCGGTCTCTGGACATCTCTCTGGTT 189
 Qy 175 GTGTTTATCTTGGTGAATAACAAGGACTCAAGAATCTGGGGAACATCTACTTCTTAAAC 234
 Db 190 GTGCTTATCTCGTAAATAATAAAGGACTCAAGCGCTGGAAATAATCTATCTTCTTAAAC 249
 Qy 235 CTGGCACTTTCAAACTGTTTCTGCTCTCCCTCGCGTTCGGGCCCACTACTGCAGCA 294
 Db 250 TTGGCAGTTTCTAACTTGTGTTTCTTGGCTTACCCTGCCCTTCTGGGCTCATGCTG- 304
 Qy 295 CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGACTCCACTCTCGGGC 354
 Db 305 -----GGGGCGATCCCATGTGTAAATAATCTCATTTGGACTGTACTTGTGGGC 351
 Qy 355 TTATACAGCAGAGGTGTTTTTCCAAACATCTCTCTCTTGTGCAAGGATACAGGGTGTTC 414
 Db 352 CTGTACAGTGAGACATTTTTTCAATTGCTTCTGACTGTGCAAAAGGTACCTAGTGTGTTT 411
 Qy 415 CAAGGGCGAC---TGGCTCCATCTTCACAGACGTGTCTGTGTGATATTGTTCGTCATC 471
 Db 412 CACAAGGGCAACTTTTTTCTCAGCCAGGAGGGTGGCCCTGTGGCATCATTTACAAGTGT 471
 Qy 472 CTGGCATGGGCCCATGGCTACTGCGCTCTCTTTGGCCGAGTCTGTGTTTATGAGCCTCG 531
 Db 472 CTGGCATGGGTAAACAGCCATCTTGGCCACTTTGCTGTGAATACGTGGTGTATTAACCTC 531
 Qy 532 ATGGAAGACAGAAACAACAAGTGTGCTTTGGCAAACTCTCACTTCTTGGCAATCGAAGCG 591
 Db 532 ATGGAAGACCAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 591
 Qy 592 CCCTCTGGAAGTACGTCTTCAGCTCAAAAATGATCATCTTGTGACTCTTCTTCTCTG 651
 Db 592 ACATTCTGGAAGCATTTTCTGACTTTAAAAAATGAACAATTTTCGGTCTTGTCTCTCC 651
 Qy 652 CTGGTTTTTATAATCTGCTGCAGCAACTCAGGAGGAGGAGGAGCTTTCAGGAGGAGCAG 711
 Db 652 TTTATTTTACATTTCTATGTGCAATGAGAAAAACATTAAGTTTCAGGAGGAGCAGAGG 711
 Qy 712 TAGCAGCTCCCAAGCGGCTCTTGTCTAATACCGGGCGTGTTCCTTTTGTGATGTGGCGCT 771
 Db 712 TATAGCTTTTCAAGCTGTTGTTTGGCATAATGATAGTCTTCTCTCTGATGTGGCGGCC 771
 Qy 772 TACAACACTGTGCTTTTCTGCTGTCTTCCAGGAACACTTGTCCCTGCAGGATGAGAG 831
 Db 772 TACAATATTGCATTTTCTCTGTCCTACTTTCAAAGAACACATTTCTCCCTGAGTGAAG 831

Db 368 CTGTACAGTGAACATTTTCAATGCTCTGACTGTGCAAGTACTAGTGTGTTTG 427
Qy 415 CAAGGGGAC--TGSCCTCCATCTTACGACAGTCTTGTGGTATGTTGGCTGATC 471
Db 428 CACAAGGGCAATTTTCTCAGCAGGAGGAGGCTCTGTGGCATCATTTACAAGTGTG 487
Qy 472 CTGCGATGGGCAATGGCTACTGCGCTCTCTTTGCGGAGTGTGTGTTTATGAGCCTCGG 531
Db 488 CTGGCATGGGTAAACAGCCATTTGCGCCACTTTGCTGTAATACGTGGTGTATTAACACCTCAG 547
Qy 532 ATGGAAGACAGAAACACAAAGTGTGCTTTTGGCAACCTCACTCTTGCCTAATGAAGCG 591
Db 548 ATGGAAGACAGAAATACAAGTGTGCAATTTAGCAGAACTCCCTTCTGCCAGCTGATGAG 607
Qy 592 CCGCTCTGGAAGTACGTTCTCAGCTCAAAATGATCATCTTGTGGTACTTGTCTTCTCTG 651
Db 608 ACATCTGGAAGCATTTCTGACCTTAAATGAACATTCGGTCTTGTCTCTCCCTA 667
Qy 652 CTGCTTTTATATCTGCTGAGGCAACTGAGGAGAGGAGGAGCTTCAGGAGAGAGAG 711
Db 668 TTTATTTTACATTTCTATGTGCAATGAGAAAAACACTAAGTTTCAGGAGCAGAGG 727
Qy 712 TACAGCTCCAAAGCGGCTCTGTCTATACGGGCGTGTCTTGTGATGTGGCGCT 771
Db 728 TATAGCCTTTTCAAGCTTGTGTTTGGCCATAATGGTAGTCTTCTCTGATGTGGCGGCC 787
Qy 772 TACAACACTGTGCTTCTGCTGCTTCCAGGAACACTTGTCCCTGCGAGGATGAGAAG 831
Db 788 TACAATATGCAATTTTCTGCTGCACTTTTCAAGAACACTTCTCCCTGAGTGTGCAAG 847
Qy 832 AGCAGCTACCACTGGAGCGCAAGTGTTCAGGTCAACAGCTGTGAGGACCACTGTC 891
Db 848 AGCAGCTACATCTGGACAAAAGTGTTCACATCACTAACTCATCGCCACCACTGTC 907
Qy 892 TGGCTAACCGCTGCTATTTGCTTGTGACCGAAGGCTTTATGAGATACCTTGGC 951
Db 908 TGCAATCAACCTCTCTGCTATGCTGCTTCTGATGGGA---CATTTAGCAATACCTCTGC 964
Qy 952 AGCCTGTTCCACGCTGCAATGATATCCCTATCAAGTAGTGTGGAGGTATCAGCAAGCG 1011
Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCTTCAACCCAGGGGCGAGTGTGCAAGGC 1024
Qy 1012 CCTCAAGGGAAGTCTATGGCAGGCGCCCATTTGAACCTGTACAGCAATTTGCAATCAAGGCAG 1071
Db 1025 ACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAACTAGCATCCACCAATGCA 1084
Qy 1072 GA 1073
Db 1085 GA 1086

RESULT 8

ABL95568
ID ABL95568 standard; cDNA; 1475 BP.

AC ABL95568;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO1873 SEQ ID NO: 15.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytosolic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX W0200208284-A2.

XX 31-JAN-2002.

XX

PF 09-JUL-2001; 2001WO-US021735.
XX 20-JUL-2000; 2000US-0219555P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220684P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006866.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.

(GETH) GENENTECH INC.

(BAKE/) BAKER K P.

(FERR/) FERRARA N.

(GERB/) GERBER H.

(GERR/) GERRITSEN M E.

(GODD/) GODDARD A.

(GODO/) GODOWSKI P J.

(GURN/) GURNEY A L.

(HILL/) HILLAN K J.

(MARS/) MARSTERS S A.

(PANG/) PAN J.

(PAON/) PAONI N F.

(STEP/) STEPHAN J F.

(WATA/) WATANABE C K.

(WILL/) WILLIAMS P M.

(WOOD/) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-171999/22.

P-PSDB; ABB95430.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.

Claim 1; Fig 15; 567pp; English.

The present invention provides the protein and coding sequences of human
PRO proteins. These are useful for treating or diagnosing a
cardiovascular, endothelial or angiogenic disorder, including cardiac
hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

Qy	952	AGCGTGTTC	CCACGGTGCAATGATATCCCTTATCAAAGTAGTGTGAGGCTATCAGCAAGCG	1011
Db	965	CGGTGTTT	TCCATCTGCGTAGTAACACCCCCACTTCAACCCAGGGGCGAGTCTGCACAAAGC	1024
Qy	1012	CCTCCAAAGG	GAAGGTGATGCGCAGGCCCATTTGAACCTGTACAGCAATTTGGCATCAAAGGCAG	1071
Db	1025	ACATCGAGG	AGAGAACTTGACCATTCACCGAGTGTAACTAGCATCCACCAATGC	1084
Qy	1072	GA	1073	
Db	1085	GA	1086	
RESULT 9				
ADD10304				
ID	ADD10304	standard;	cdNA; 1475 BP.	
XX	AC			
XX	AC	ADD10304;		
XX				
DT	01-JAN-2004	(first entry)		
XX				
DE	Human secreted/transmembrane	PRO polypeptide	cdNA #8.	
XX				
KW	ss; gene; human; secreted protein;	transmembrane protein;		
KW	cardiovascular disorder; endothelial	disorder; angiogenic disorder;		
KW	myocardial infarction; cardiac hypertrophy;	trauma; cancer;		
KW	age-related macular degeneration;	angiogenesis;		
KW	endothelial cell apoptosis; smooth	muscle cell growth;		
XX	endothelial cell tube formation.			
XX				
OS	Homo sapiens.			
XX				
PN	US2003105011-A1.			
XX				
PD	05-JUN-2003.			
XX				
PF	16-AUG-2002; 2002US-00223084.			
XX				
XX	15-SEP-2000; 2000US-0232887P.			
PR	20-JUN-2001; 2001WO-US019692.			
PR	09-JUL-2001; 2001WO-US021735.			
PR	20-FEB-2002; 2002US-00081056.			
XX				
PA	(GETH) GENENTECH INC.			
XX				
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;			
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;			
PI	Watanabe CK, Williams PM, Wood WI, Ye W;			
XX				
XX	WPI; 2003-810831/76.			
DR	P-PSDB; ADD10305.			
XX				
PT	New isolated nucleic acid encoding a secreted and transmembrane			
XX	polypeptide for treating a cardiovascular, endothelial, or angiogenic			
PT	disorder in a mammal, such as cancer or age-related macular degeneration.			
XX				
XX	Claim 2; SEQ ID NO 15; 493pp; English.			
XX				
CC	The invention relates to an isolated nucleic acid encoding a secreted and			
CC	transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded			
CC	by the nucleic acid, or an agonist or antagonist, is used to treat a			
CC	cardiovascular, endothelial, or angiogenic disorder in a mammal,			
CC	preferably a human. The human may have suffered a myocardial infarction			
CC	or has cardiac hypertrophy, trauma, a cancer, or age-related macular			
CC	degeneration. The cardiac hypertrophy is characterised by the presence of			
CC	an elevated level of bFGF-2 alpha. A PRO polypeptide, given in the			
CC	specification, or an agonist is used to inhibit or stimulate endothelial			
CC	cell growth in a mammal. PRO21 or an agonist is used to induce cardiac			
CC	hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.			
CC	PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO			
CC	polypeptide, given in the specification, or an agonist is used to			
CC	stimulate or inhibit smooth muscle cell growth, or to induce endothelial			


```
CC PRO polypeptide of the invention.
XX
SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match          39.0%; Score 422; DB 10; Length 1475;
Best Local Similarity 65.5%; Pred. No. 1.3e-116;
Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

QY 1 ATGGATAACTACACAGTGGCCCGGACGATGAATATATGATGCTCTAATCTTAGACGACTAC 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 29 ATGGCCAATTTACACGCTGGCCAGGAGATGAATATGATGCTCTAATCTTAGACGACTAC 85
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CTGGACAACAGTGGCCGACCAAGTT-----CGGCCCGCCGAGTTCCTCTCCCGCCAG 114
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 86 CTGGAGCGCATGAGGACGAGCAATGTGACAAGTATGACGCCGAGCACTCTCAGCCGAG 145
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 CAGGTGCTGCAAGTTCTGCTGCGCGGTGTTTTCGCGGTGCTCTTGGACAACGTCGTGGCG 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 146 CTGGTGCCATCACTCTGCTCTGCTGTTGTTGTGATCGGTCTCTGGACAATCTCTGGTT 205
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 GTGTTTATCTTGTGAATACAAAGNACTCAAGAACTCTGGGAACATCTACTTCTTAAC 234
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 206 GTGCTTATCTGTGAATATNAAGGACTCAAAACGCGTGGAATAATCTATCTTCTTAAC 265
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 CTGGCACTTTCAAACTGTGTTTCTGCTTCCCTGCGCTCTGCGGCCATCTACTGCGACA 294
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 266 TTGGCAGTTTCAACTGTGTTTCTGCTTACCTGCGCTTCTGGGCTCATGCTG----- 320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 CACGGGGAAGCCCTGCAACGGGACCTGTAAAGTTCTTGTGCGACTCCAACCTCTCGGGC 354
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 321 -----GGGCGATCCCATGTGTAAATAATCTCATTTGGACTGTACTTCTGTTGGC 367
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 TTATACAGCAGGTGTTTTCACACATCTCTCTCTTGTGCAAGATACAGGGTGTGTTTCC 414
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 CTGTACAGTGAGACATTTTTCATATGCTTCTGACTGTGCAAAAGTACCTAGTGTGTTG 427
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 CAAGGGCGAC---TGGGCTCCATCTTCACGACAGTGTCTGTGTTATGTTGTGCGTGCATC 471
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 CACAGGGCAACTTTTCTCAGCCAGGAGAGGGTGCCTGTGGCATCATTAAGTGTGTC 487
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 CTGGCATGGCCATGAGTACTGCGCTCTCTTTGCCGAGTCTGTGTTTATGAGCTCGG 531
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 CTGGCATGGGTAAACAGCCATCTTGGCCACTTTCCTGAATACGCTGTTTATAAACTCAG 547
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 ATGGAAGACAGAAACACAGTGTGCTTTGGCAACCTCACTTCTTGCATCGAAGCG 591
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 548 ATGGAAGACAGAAATACAAAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAG 607
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 592 CCGCTCTGGAAGTACGTTCTGAGCTCAAAAATGATCATCTGTGTAATCTGTTTCTCTG 651
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 608 ACATCTGGGAAGCATTTTCTGACTTTTAAATAAGACATTTCTGCTTCTGCTCCCTTA 667
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 652 CTGGTTTTTATATCTGCTCAGGCAACTGAGGAGAGGAGAGTTCAGGAGAGACAG 711
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 TTTATTTTACATTTCTCTATGTGCAATGAGAAAAACATAAGTTTCAGGAGCAGAGG 727
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 712 TAGCACTCCACAGCGGCTTGTGTCATACCGGGGTGTTCTTTTGTGTTGGCGCCT 771
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 728 TATAGCCTTTTCAAGCTGTTTGTGCAATAATGATGTTCTTCTGATGTGGCGGCC 787
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 772 TACAACACTGTGCTTTTCTGCTGCTTCCAGAACACTTGTCCCTGCGAGGATGAGAAG 831
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 788 TACAAATATGCAATTTTCTGCTTCCACTTTCAAGAACACTTCTCCCTGAGTGAAGTGCNAG 847
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 832 AGCAGCTACCACTGAGCAAGTGTTCAGGTCAACAGCTGTGTAGGACCAACCACTGC 891
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 848 AGCAGCTACAACTGGAACAAAAGTGTTCACATCACTAAACTCATCGCCACACCCACTGC 907
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 892 TGGCTCAACCCGCTGCTATTTGCTTCTTGAACCGGAGCCCTTTATGATACCTTCGC 951
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 908 TGCATCAACCCCTCTCTGTATGCGTTTCTTGTATGGGA---CATTTAGCAAAATACCTTCGC 964
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 952 AGCCTGTTCCACGGGTGCAATGATATCCCTCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG 1011
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC 1024
1012 CTCTCAAGGGAAGGTCTATGCGAGGCCCATTTGAACTGTACAGCAATTTGCATCAAGGCAG 1071
1025 ACATCGAGGGAAGAACCTGACCATTCACCGAAGTGTAAACTAGCATCCACCAAAATGCAA 1084
1072 GA 1073
1085 GA 1086

RESULT 11
ADD37057
ID ADD37057 standard; cDNA; 1475 BP.
XX
AC ADD37057;
AC AC
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide cDNA #8.
XX
KW ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105012-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223088.
XX
PR 15-SEP-2000; 2000US-0232887P.
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2003-829354/77.
DR P-PSDB; ADD37058.
XX
PT New isolated nucleic acids encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS Claim 2; SEQ ID NO 15; 492pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a secreted and
XX transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
XX by the nucleic acid, or an agonist or antagonist, is used to treat a
XX cardiovascular, endothelial, or angiogenic disorder in a mammal,
XX preferably a human. The human may have suffered a myocardial infarction
XX or has cardiac hypertrophy, trauma, a cancer, or age-related macular
XX degeneration. The cardiac hypertrophy is characterized by the presence of
XX an elevated level of Pgf-2 alpha. A PRO polypeptide, given in the
XX specification, or an agonist is used to inhibit or stimulate endothelial
XX cell growth in a mammal. PRO149 or an agonist is used to induce cardiac
XX hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
XX PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
XX polypeptide, given in the specification, or an agonist is used to
XX stimulate or inhibit smooth muscle cell growth, or to induce endothelial
XX cell tube formation. The present sequence represents a cDNA encoding a
XX PRO polypeptide of the invention.
```

[illegible]

SQ	Sequence	1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;	
	Query Match	39.0%; Score 422; DB 12; Length 1475;	
	Best Local Similarity	65.5%; Pred. No. 1.3e-116;	
	Matches	709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;	
QY	1	ATGGATAACTACACAGTGGCCCGGACGATGAATATATGATCTCTTAATCTTTAGACGACTAC	60
DB	29	ATGGCCAAATTACACGCTGGCACACAGGATGAATATGATCTCC---TCATAGAAGTGAA	85
QY	61	CTGGACAAAGTGGCCCGGACCAAGTT-----CCGGCCCCCGAGTTCTCTCCCCCAG	114
DB	86	CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCGGCACTCTCAGGCCAG	145
QY	115	CAGGTGCTGACGTTCTGCTGGCGGTGTTTGGCGTGTCTTTGGACACGTTGCTGGCG	174
DB	146	CTGTTGCCATCACTCTGCTCTGCTGTGTTGTGATGGTGTCTTGGACAATCTCTTGTT	205
QY	175	GTGTTTATCTTGTGTAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTCTAAAC	234
DB	206	GTGCTTATCTGTGTAATATAAGGACTCAACGCTGGAAATATCTATCTTCTTAAC	265
QY	235	CTGGCACTTTCAACCTGTGTTCTGCTTCCCTGCGCTTCTGGGCCCACTATCGAGCA	294
DB	266	TTGGCAGTTTCTAACTTGTGTTCTTGTCTTACCCTGCCCCCTTCTGGGCTCATGCTG----	320
QY	295	CACGGGGAAGCCCTGCAACGGGACCTGTAAAGTTCTTTCGAGCTCCACTCTCTGGGC	354
DB	321	-----GGGGCGATCCCATGTGTAAATTTCTCAITGGACTGTACTTCTGTTGGGC	367
QY	355	TTATACAGCGAGTGTGTTTCCAAATCTCTCTCTGTGCAAGATACAGGGTGTGTTTCC	414
DB	368	CTGTACAGTGAGACATTTTCAATGCTTCTGACTGTGCAAGGTACTAGTGTGTTTGG	427
QY	415	CAAGGGCGAC---TGGCCTCCATCTTTCACAGAGTGTCTTGTGTAATTTGTTGCGTCATC	471
DB	428	CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCCCTGTGGCATCATTAAGTGTG	487
QY	472	CTGGCATGGCCATGGCTACTGCGCTCTCTTTGCGCGAGTCTGTGTTTATGAGCCTCG	531
DB	488	CTGGCATGGGTAAACAGCCATTTCTGGCCACTTTTCCCTGAATACGTGTTTATAAACCTCAG	547
QY	532	ATGGAAGACAGAAACACAAGTGTGCTTTGGCAAACTCACATCTTTCGCCAATCGAAGCG	591
DB	548	ATGGAAGACAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGTATGAG	607
QY	592	CCGCTCTGGAAGTACGTTCTGAGCTCAAAAATGATCATCTTGTGTAATCTGTTTCTCTG	651
DB	608	ACATTTCTGGAAGCATTTTCTGACTTTTAAATAATGAACATTTTCGGTCTCTTGTCCCTT	667
QY	652	CTGGTTTATATCTGCTCGAGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	711
DB	668	TTTATTTTATCAATTTCTATGTGCAATAGAGAAAACACTAAGGTTTCAGGGAGCAGAGG	727
QY	712	TACGACTCCACAAGCGGCTTGTGTCATAACGGGCTGTCTTCTTTGATGTGGGCGCT	771
DB	728	TATAGCTTTTCAAGCTGTTTGTGGCATTAATGGTAGTCTTCTCTGATGTGGGGGCC	787
QY	772	TACAACACTGTGCTTTTCTGCTCTGCTTTCCAGGAACACTTGTCCCTCGCAGGATGAGAAG	831
DB	788	TACAATATTGCAATTTTCTGCTCCACTTTTCAAGAACACTTCTCCCTGAGTGACTGCAAG	847
QY	832	AGAGCTACCACTTGGACGCAAGTGTTCAGGTACACAGCTGTAGGACCACTCCACTGC	891
DB	848	AGCAGCTACAATCTGGACAAAAGTGTTCACATCACTAAATCTATGCCACCACTCCACTGC	907
QY	892	TGGCTCAACCCGCTGCTCTATTGCTTCTTACGCGGAAGCCCTTTATGATACCTTCGCG	951
DB	908	TGATCAACCCCTCTCTGTAATGGTCTTCTGATGGGA---CATTTAGCAATACCTCTGC	964
QY	952	AGCCTGTTCACGGGTGCAATGATATCCCTCTATCAAAAGTAGTGGAGGCTATACGAAGCG	1011
DB	965	CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGC	1024
QY	1012	CTTCCAGGAGAGGTCTATGGAGGCCCATTTGACTGTACAGCAATTTGCATCAAGGCAG	1071
DB	1025	ACATCCAGGGAAGAACCTGACCATTTCCCGAAGTGTAACTAGCATCCACCAATGCAA	1084
QY	1072	GA 1073	
DB	1085	GA 1086	
RESULT 13			
ID	ADH43448		
AD	ADH43448	standard; cDNA; 1475 BP.	
AC	ADH43448;		
DT	25-MAR-2004	(first entry)	
XX	Human PRO polynucleotide #8.		
XX	Human; PRO; gene; ss; cardiovascular disorder; endothelial disorder;		
KW	angiogenic disorder; endothelial cell growth; cardiac hypertrophy;		
KW	cell apoptosis; cell tube formation; angiogenesis;		
KW	smooth muscle cell growth; myocardial infarction; trauma; cancer;		
KW	age-related macular degeneration; cytostatic; cardiant;		
KW	cerebroprotective; ophthalmological; vulnary.		
OS	Homo sapiens.		
XX	US2003224984-A1.		
PN	04-DEC-2003.		
XX	26-NOV-2002; 2002US-00305654.		
PF	20-JUN-2001; 2001WO-US019692.		
XX	(GETH) GENENTECH INC.		
XX	Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;		
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;		
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;		
XX	WPI: 2004-042166/04.		
DR	P-PSDB; ADH43449.		
XX	New PRO polypeptides and nucleic acids encoding the polypeptides, useful		
PT	for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,		
PT	or age-related macular degeneration.		
XX	Claim 2; SEQ ID NO 15; 492pp; English.		
PS	The invention relates to human PRO polypeptides and the PRO		
XX	polynucleotides encoding them. The invention also relates to treating		
CC	cardiovascular, endothelial or angiogenic disorders in mammals,		
CC	inhibiting endothelial cell growth, stimulating endothelial cell growth,		
CC	inducing cardiac hypertrophy, cell apoptosis or cell tube formation and		
CC	stimulating angiogenesis or smooth muscle cell growth by administering		
CC	polypeptides of the invention. The PRO polypeptides and polynucleotides		
CC	are useful for treating cardiovascular, endothelial or angiogenic		
CC	disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,		
CC	cancer or age-related macular degeneration. The PRO polynucleotides are		
CC	useful as hybridisation probes in chromosome and gene mapping and in		
CC	generating antisense RNA and DNA, and for chromosome identification and		
CC	tissue typing. The PRO polypeptides and polynucleotides are also useful		
CC	in gene therapy and as molecular weight markers for protein		
CC	electrophoresis purposes. This sequence represents a human PRO		
CC	polynucleotide of the invention.		
XX	Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;		
SQ	Query Match	39.0%; Score 422; DB 12; Length 1475;	
	Best Local Similarity	65.5%; Pred. No. 1.3e-116;	

		Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;			
Qy	1	ATGATAACTACAGTGGCCCGACGATGAATATGATGCTCTTACGAGCTAC	60		
Db	29	ATGCGCAATTACAGCTGGCCAGAGATGAATATGATGCTCTTACGAGCTAC	85		
Qy	61	CTGACAAACAGTGGCCCGACGAGTT-----CGGCCCGCGAGTTCTCTCCCGCCAG	114		
Db	86	CTGGAGAGCGATGAGCGAGAGCAATGTGCAAGTATGACGCCCGACGCTCTCAGCCCGAG	145		
Qy	115	CAGTGTCTGAGTCTGCTGGCGGCTGTTGGGGTGGTCTCTTGGACAAAGTGTGTCGG	174		
Db	146	CTGTGCGCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	205		
Qy	175	GTGTTTATCTTGGTGAATACAAAGGACTCAAGAACTCGGGGAAACATCTCTCTTAAC	234		
Db	206	GTGTTTATCTTGGTGAATATGAAGGACTCAAGCGGTGGAAATATCTCTCTTAAC	265		
Qy	235	CTGGCACTTTCAAACTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	294		
Db	266	TTGGCAGTTTCTAACTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	320		
Qy	295	CACGGGAAACCTCGCAAGCGGACCTGTAAAGTTCTTGTGGACTCCACTCTCTCGGGC	354		
Db	321	-----GGGGCGATCCCATGTGTAAATTTCTCATTTGGACTGTACTCTCTGGGC	367		
Qy	355	TTATACAGGAGTGTGTTTCCAAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	414		
Db	368	CTGTACAGTGAACATTTTCAATGTCCTCTGACTGTGCAAGGACTCTAGTGTGTTTG	427		
Qy	415	CAAGGGCGAC---TGGCCTCCATCTTCAACAGAGTGTCTGTGTATTTGTCGTGCATC	471		
Db	428	CACAAGGCACTTTTCTCAGCAGGAGGAGGTGCCCTGTGCAATATTACAAGTGTG	487		
Qy	472	CTGGCATGGCCATGGCTACTGCGCTCTCTTTGCGCGAGTCTGTGTTTATGAGCCTCGG	531		
Db	488	CTGGCATGGGTAAACAGGCAATCTCGGCCACTTTGCTGTAATACGTGGTGTATATAACCTCAG	547		
Qy	532	ATGGAAGACAGAAACACAGTGTGCTTTGGCAAACTCACTCTTGGCAATCGAAGCG	591		
Db	548	ATGGAAGACCAAAATACAGTGTGCAATTTAGCAGAACTCCCTTCTGCGCAGCTGATGAG	607		
Qy	592	CCGCTCTGGAAGTACGTTCTGACGCTCAAAATGATCATCTTGTGTTCTTTTCTCTG	651		
Db	608	CAATCTGGAAGCATTTCTGACTTAAATGAACATTTGCTGCTCTCTCTCTCTCTCTCT	667		
Qy	652	CTGTTTTTATAATCTGCTGAGGCAACTGAGGAGAGGAGAGCTTCAGGAGAGACAG	711		
Db	668	TTTATTTTATCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGAGAGAGAGG	727		
Qy	712	TACGACCTCCACAGCGGCTTGTGATACGCGGCTGTTCTCTTTTGTGTTGGCGCCT	771		
Db	728	TATAGCCTTTTCAAGCTGTTTTTGGCAATATGATGCTCTCTCTCTGATGTTGGCGGCC	787		
Qy	772	TACAACACTGTCT	831		
Db	788	TACAATATGCAATTTTCT	847		
Qy	832	AGCAGTACCACTGGAGCGAAGTGTTCAGGTCAACAGCTGGTAGCGACACCCACTGC	891		
Db	848	AGCAGTACCACTGGAGCAAAAGTGTTCACATCACTAAACTCATCGCCACACCCACTGC	907		
Qy	892	TGCTCAACCGCTGCTCTATTTGCTTCTTGGCGGAGGCTTTTATGATACCTTCGC	951		
Db	908	TGCTCAACCGCTCTCTCTGATGCTGCTTCTTGTATGCGA---CATTTAGCAATACCTCTGC	964		
Qy	952	AGCCTGTTTCCACGCTGCAATGATATCCCTTATCAAAAGTATGAGGCTATCAGCAAGC	1011		
Db	965	CGCTGTTTCCATCTGCGTAGTAAACACCCCACTTCAACCCAGGGGAGTCTGCAACAGC	1024		
Qy	1012	CTTCAAGGAGGTCTAGCGAGGCCCATTTGAATCTGACAGCAATTTGCAATCAAGGCAG	1071		
Db	1025	ACATCGAGGAGAAACCTGACCATTTCCACCGAAGTGTAAACTAGCATCCCAATGCAA	1084		

Qy 1072 GA 1073
Db 1085 GA 1086

RESULT 14
ADK82793
ID ADK82793 standard; cDNA; 1475 BP.

AC ADK82793;
XX 20-MAY-2004 (first entry)
XX Human PRO polynucleotide #8.

Human; PRO; gene; ss; cardiovascular disorder; endothelial disorder;
angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
cell apoptosis; cell tube formation; angiogenesis;
smooth muscle cell growth; myocardial infarction; trauma; cancer;
age-related macular degeneration; cytosstatic; cardiant;
cerebroprotective; ophthalmological; vulnerary.

Homo sapiens.

US2004043927-A1.

04-MAR-2004.

20-FEB-2002; 2002US-00081056.

19-SEP-1997; 97US-00933821.
29-JAN-1998; 98US-00015089.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98WO-US019177.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
19-NOV-1998; 98US-00180997.
01-DEC-1998; 98WO-US025108.
22-DEC-1998; 98US-00218517.
05-JAN-1999; 99WO-US000106.
12-FEB-1999; 99US-00214186.
03-MAR-1999; 99US-00254311.
08-MAR-1999; 99WO-US005028.
09-MAR-1999; 99US-00254460.
12-MAR-1999; 99US-00267213.
12-APR-1999; 99WO-US012252.
02-JUN-1999; 99US-00332928.
14-JUN-1999; 99US-00380137.
14-JUN-1999; 99US-00380138.
25-AUG-1999; 99US-00380139.
01-SEP-1999; 99WO-US020111.
08-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
15-SEP-1999; 99WO-US023089.
03-OCT-1999; 99US-00403154.
18-OCT-1999; 99US-00403296.
18-OCT-1999; 99US-00403297.
10-NOV-1999; 99US-00421741.
12-NOV-1999; 99US-00423843.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028564.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030999.

Db 608 ACATTTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTTCGGTTCTTGCTCTCCCCCTA 667
 Qy 652 CTGTTTTTAAATCTGCTGAGCACTGAGGAGGAGAGCTTCAGGAGAGACAG 711
 Db 668 TTTATTTTACATTTCTCTATGTGCAATGAGAAAAACACTAAGGTTTCAGGAGACAGAG 727
 Qy 712 TACGACCTCCCAAGCGGCTCTGTCTATACGCGGCTGTTTCTTTTGATGTGGCGGCT 771
 Db 728 TATAGCTTTTCAAGCTTGTCTTTCGCAATATGTAATCTTCTGATGTGGCGGCT 787
 Qy 772 TACAACACTGTCTTCTGCTGCTTTCAGGAGACACTGTCTGCTGAGAGAGAG 831
 Db 788 TACAATATTGCAATTTTCTGCTGCACTTTCAAGAGAACACTTCTCCCTGAGTGCAG 847
 Qy 832 AGCAGCTACCACTGGAGCAAGTGTTCAGGTTCACACAGCTGTAGCGACCACTGC 891
 Db 848 AGCAGCTACAATCTGGACAAAGTGTTCACATCACTAACTATCGCCACCACTGC 907
 Qy 892 TGCCTCAACCGCTGCTCTATTTGCTTCTTGACCGGAGGCTTTATGAGATACCTTGC 951
 Db 908 TGCATCAACCTCTCTCTGTATGCTTCTTGATGGA---CATTTAGCAATACCTCTGC 964
 Qy 952 AGCTGTCTCCACCGTGAATGATATCCCTATCAAGTAGTGAAGGTATCAGAACGC 1011
 Db 965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCGGGGCGAGTGTGCAAGGC 1024
 Qy 1012 CTTCAAGGAGGTATGCGAGCGCCATTCAGCTGACAGCAATTTGCATCAAGGCAG 1071
 Db 1025 ACATCGAGGAGAACTGACATTCACCGAAGTGTAACTAGCATCCCAATGCA 1084
 Qy 1072 GA 1073
 Db 1085 GA 1086

RESULT 15

ABZ42782
 ID ABZ42782 standard; DNA; 1645 BP.

XX AC ABZ42782;

XX DT 04-MAR-2003 (first entry)

XX DE Human chemokine receptor-like 2 nucleotide SEQ ID NO:353.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PP 19-DEC-2001; 2001WO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burner GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

DR P-PSDB; ABP81934.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 (GPCR), useful for diagnosing and designing drugs for treating conditions
 in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 autoimmune diseases.

XX Disclosure, Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (1) comprising, (a)
 any one of 1501 sequences (see ABP819 to ABP83619) of 12-44 amino
 acids. Also described: (1) an assay for the detection of a particular G
 protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 and (2) an isolated antibody having high specificity and high affinity or
 avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 antibody against a particular GPCR, and in the production of specific
 antibodies. The peptides and antibodies are also useful for detecting the
 presence or absence of corresponding GPCRs. The antigenic peptides for
 GPCRs and antibodies are useful for diagnosing and designing drugs for
 treating immune-related diseases, growth-related diseases, cell
 regeneration-related disease, immunological-related cell proliferative
 diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 atherosclerosis, bacterial, fungal, protozoan or viral infections,
 osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 inflammation, allergies, Crohn's disease, diabetes, graft versus host
 disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 anxiety, depression, schizophrenia, dementia, mental retardation, memory
 loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 any other disorder in which GPCRs are involved. The antibodies may be
 used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 GPCR proteins given in ABP81675 to ABP82018, which are used in the
 exemplification of the present invention

XX SQ Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other;

Query Match 39.0%; Score 422; DB 8; Length 1645;

Best Local Similarity 65.5%; Pred. No. 1.3e-116;

Matches 709; Conservative 0; Mismatches 340; Indels 33; Gaps 5;

Qy 1 ATGGATAACTACACAGTGGCCCGGACGATGATATGATGTCCTTAATCTTAGACGACTAC 60
 Db 203 ATGGCCAAATTACACGCTGGCCACGACGAGGATGATGATGTCC---TCATAGAGGTGAA 259
 Qy 61 CTGGACAAACAGTGGCGCGACCAAGTT-----CGGCCCCCGAGTCTCTCCCCCAG 114
 Db 260 CTGGAGAGCGATGAGGACGAGCAATGTGACAAGTATGACGCCCGGCACTCTAGCCCCG 319
 Qy 115 CAGTGTCTGCAAGTCTCTGCGCGGTGTTTGGGTGGTCTCTTTGGACAACTGCTGGCG 174
 Db 320 CTGGTGCATCACTCTGCTCTGCTGTTTGTGATCGGTGCTGGACAATCTCTGGTT 379
 Qy 175 GTGTTTATCTTGTGAATAACAAGGACTCAGAACTCTGGGACATCTACTTCTTAAC 234
 Db 380 GTGCTATCTCTGTAATAATAAAGGACTCAACGCGTGGAAAAATATCTATCTTCTAAC 439
 Qy 235 CTGSCACTTTCAAACTGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294
 Db 440 TTGSCAGTTTCTAACTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 494
 Qy 295 CACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTCTTGTGCGACTCCACTCTCGGGC 354
 Db 495 -----GGGCGGATCCCATGTGTAAATTTCTCATTTGAGTGTACTTCTGTTGGC 541
 Qy 355 TTATACAGCGAGGTGTTTTCACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414
 Db 542 CTGTACAGTGAACATTTTCAATTTGCTTCTGACTGTGCAAGGTACCTAGTGTGTTT 601
 Qy 415 CAAGGGGAC---TGGCTCCATCTTCCAGCACAGTGTCTTGTGTATTGTTGCGTGCATC 471
 Db 602 CACAGGGCAACTTTTCTCAGCCAGGAGGAGGTGCCCTGTGTCATCATTTACAGTGT 661
 Qy 472 CTGGCATGGGCCCATGGCTACTGCGCTCTCTTTGCGCGAGTCTGTGTTTATGAGCCTCG 531

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: June 18, 2005, 06:34:54 ; Search time 637.224 Seconds
(without alignment)

9615.040 Million cell updates/sec

Title: US-10-623-472-31

Perfect score: 1035

Sequence: 1 atggcaattacacgtgcg.....accattccacgaagtgttaa 1035

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1035	100.0	1035	6	ABSS2092 Human CCR
2	1035	100.0	1547	2	AAV15419 Human mac
3	1035	100.0	1547	2	ABX95937 Human mon
4	1035	100.0	1547	12	ADG67844 Human CDN
5	1032.2	99.7	1646	13	ADQ38349 Human SNP
6	1032.2	99.7	1776	13	ADQ38350 Human SNP
7	1031.8	99.7	1140	12	ACH89585 Human gen
8	1031.8	99.7	1475	6	ABL88079 Human pro
9	1031.8	99.7	1475	6	ABL95568 Human ang
10	1031.8	99.7	1475	10	ADD10304 Human sec
11	1031.8	99.7	1475	10	ADD11264 Human sec
12	1031.8	99.7	1475	10	ADD37057 Human sec
13	1031.8	99.7	1475	12	ADA41265 Human sec
14	1031.8	99.7	1475	12	ADH43448 Human PRO
15	1031.8	99.7	1475	12	ADK82793 Human PRO
16	1031.8	99.7	1645	8	ABZ42782 Human che
17	1031.8	99.7	1645	11	ADN95729 Human BEC
18	1031.8	99.7	1645	13	ADP24442 PRO polyp
19	1031.8	99.7	1645	13	ADSF5309 Human CCR
20	1031.8	99.7	1698	12	ADP13564 Renal cel

21	1031.8	99.7	143040	11	ABD20648	Abd20648 Human pul
22	1031.8	99.7	143067	11	ABD20815	Abd20815 Human pul
23	1031.8	99.7	143068	3	AAA34983	Aaa34983 Human ade
24	1031.8	99.7	143068	3	AAA35150	Aaa35150 Human ade
25	1031.8	99.7	143068	3	AAF21272	Aaf21272 Human low
26	1031.8	99.7	143068	3	AAF21105	Aaf21105 Human low
27	1031.8	99.7	143068	3	ABL68124	AbL68124 Ovary can
28	1031.8	99.7	143068	6	ABT11034	ABt11034 Human bre
29	1031.8	99.7	143068	10	ABZ96966	Abz96966 Human nuc
30	1031.8	99.7	143068	10	ABZ96799	Abz96799 Human nuc
31	1031.8	99.7	149412	3	AAA35151	Aaa35151 Human ade
32	1031.8	99.7	152739	11	ABD20816	Abd20816 Human pul
33	1031.8	99.7	152740	3	AAF21273	Aaf21273 Human low
34	1031.8	99.7	152740	10	ABZ96967	Abz96967 Human nuc
35	1030.2	99.5	1035	12	ADO30063	Ado30063 Human GPC
36	1029.8	99.5	1270	10	ACA56158	Aca56158 Human sig
37	1029.8	99.5	1270	12	ADI55954	Adi55954 Human pol
38	1029.4	99.5	1316	2	AAT99543	Aat99543 Human che
39	1028.8	99.4	1251	11	ADP03560	Adp03560 Human GPC
40	973.4	94.0	1050	2	AAV04641	Aav04641 cDNA enco
41	973.4	94.0	1050	6	AAS17436	Aas17436 Human CDN
42	973.4	94.0	1050	6	AAD42836	Aad42836 Human G-p
43	695.8	67.2	7644	6	ABL32885	AbL32885 Human imm
44	651	62.9	7644	6	ABL32884	AbL32884 Human imm
45	505.2	48.8	588	5	AAF93267	Aaf93267 Lung endo

ALIGNMENTS

RESULT 1
ABS52092
ID ABS52092 standard; cDNA; 1035 BP.
XX
AC ABS52092;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CCR12 cDNA.
XX
KW Human; CCR12; gene; ss; chemokine receptor; CCRAM-B; MCP-1; HEK cell;
KW Monocyte Chemoattractant Protein-1; brain glial cell; ischaemia; asthma;
KW inflammatory disease; degenerative brain disease; Alzheimer's disease;
KW multiple sclerosis; neurodegenerative disease; neuroinflammatory disease;
KW allergic encephalitis; chronic obstructive pulmonary disease;
KW obstructive airway disease; neuroprotective; antiinflammatory.
XX
OS Homo sapiens.
XX
XX WO200257779-A2.
XX
XX 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-NL000039.
XX
PR 18-JAN-2001; 2001EP-00200181.
XX
PA (UYGR-) RIJKSUNIV GRONINGEN.
XX
XX Boddeke BHWGM, Biber K;
XX
XX WPI; 2002-599725/64.
XX
PT Identifying compounds for treating inflammatory or degenerative brain
PT diseases, comprises testing the compound for its capacity to modulate or
PT mimic Monocyte Chemoattractant Protein-1 binding with a chemokine
PT receptor.
XX
PS Disclosure; Fig 8; 45pp; English.
XX
CC The invention relates to identifying a candidate drug compound comprising
CC testing the compound for its capacity to modulate or mimic Monocyte
CC Chemoattractant Protein-1 (MCP-1) binding with a chemokine receptor

CC capable of being expressed on brain glial cells and is known in the mouse
CC as L-CCR or in humans as CCR4-B. The chemokine receptor expressed in a
CC cultured cell comprising the cell transfected with a nucleic acid and a
CC HEK cell, is useful in identifying a candidate drug compound for treating
CC inflammatory or degenerative brain disease, e.g. ischaemia, Alzheimer's
CC disease or multiple sclerosis. The agonist or antagonist is useful in the
CC preparation of the pharmaceutical composition useful in treating
CC neurodegenerative and neuroinflammatory diseases such as allergic
CC encephalitis and chronic obstructive pulmonary disease and obstructive
CC airway diseases such as asthma. This sequence represents human CCR4-B
CC cDNA, also known as CCR12
SQ Sequence 1035 BP; 255 A; 255 C; 228 G; 297 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 6; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCAATTACACGCTGGCCACGAGGATGAATATGATGCTCTCATAGAAGTGAACCTG 60
DB 1 ATGCCCAATTACACGCTGGCCACGAGGATGAATATGATGCTCTCATAGAAGTGAACCTG 60
QY 61 GAGAGCGATGAGGAGGAGCAATGTGCAAGTATGAGCGCCAGGCACTCTCAGCCAGCTG 120
DB 61 GAGAGCGATGAGGAGGAGCAATGTGCAAGTATGAGCGCCAGGCACTCTCAGCCAGCTG 120
QY 121 GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CTATCTCTGTAATAATATGAAGGACTCAAGCGGTGGAATAATATCTATCTCTAAACTTG 240
DB 181 CTATCTCTGTAATAATATGAAGGACTCAAGCGGTGGAATAATATCTATCTCTAAACTTG 240
QY 241 GCAGTTTCTAACTTGTGTTCTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCAGTTTCTAACTTGTGTTCTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 CCATGTGTAAATATCTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 CCATGTGTAAATATCTCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 AATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 AATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CTGGCCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CTGGCCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TGTGCAATTTAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TGTGCAATTTAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 ACTTTAAATTTAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 ACTTTAAATTTAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GTGCAATTTAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 GTGCAATTTAGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 TTTGCGGTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 TTTGCGGTAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TCCACTTTTCAAGAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 TCCACTTTTCAAGAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 841 AGTGTTCACATCACTAACTCATCGCCACACCCACTGCTGTCATCAACCCCTCTCTCTGTAT 900
DB 841 AGTGTTCACATCACTAACTCATCGCCACACCCACTGCTGTCATCAACCCCTCTCTCTGTAT 900
QY 901 GCGTTTCTTGTATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
DB 901 GCGTTTCTTGTATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
QY 961 ACCCACTTCAACCCAGGGGCGAGTCTGCACAGGACATCGAGGGAAGAACCTGACCAT 1020
DB 961 ACCCACTTCAACCCAGGGGCGAGTCTGCACAGGACATCGAGGGAAGAACCTGACCAT 1020
QY 1021 TCCACCGAAGTGTAA 1035
DB 1021 TCCACCGAAGTGTAA 1035
RESULT 2
AAV15419
ID AAV15419 standard; cDNA; 1547 BP.
XX
AC AAV15419;
XX AC
DT 11-JUN-1998 (first entry)
XX
DE Human macrophage/dendritic cell chemokine receptor encoding cDNA.
XX
KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor;
KW dendritic cell; macrophage; inflammation; asthma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 49..1119
FT FT /*tag= a
FT FT /product= "M/DC CR"
FT FT /note= "macrophage/dendritic cell chemokine receptor"
XX
PN W09801557-A2.
XX
PD 15-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US010819.
XX
PR 05-JUL-1996; 96US-00675814.
PR 11-OCT-1996; 96US-0028329P.
PR 04-JUN-1997; 97US-0048593P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gish KC, Schall TJ, Vicari A, Zlotnik A, Wang W;
XX
DR WPI; 1998-101054/09.
XX
DR P-PSDB; AAW48087.
XX
PT Novel chemokines, e.g. thymus expressed chemokine - used for treating
PT inflammatory conditions including asthma.
XX
PS Claim 5; Page 95-97; 202pp; English.
XX
CC The present sequence encodes human macrophage/dendritic cell chemokine
CC receptor. Antibodies which bind to the protein can be used in detecting
CC or diagnosing various immunological conditions related to expression of
CC the protein. The nucleic acid can be used for screening and isolating DNA
CC clones for the chemokines, especially from other species. The chemokine
CC can be used in the treatment of conditions associated with abnormal
CC physiology or development, including inflammatory conditions such as
CC asthma
XX
SQ Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 2; Length 1547;

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGCCCAATTACACGCTGGCAGACGATGAATATATGATGCTCTCATAGAAGGTGAACCTG	60
Db	85	ATGCCCAATTACACGCTGGCAGACGATGAATATATGATGCTCTCATAGAAGGTGAACCTG	144
Qy	61	GAGAGCGATGAGGAGGAGCAATATGACAAAGTATGACGCCAGGACACTCTCAGCCAGCTG	120
Db	145	GAGAGCGATGAGGAGGAGCAATATGACAAAGTATGACGCCAGGACACTCTCAGCCAGCTG	204
Qy	121	GTGCGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
Db	205	GTGCGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	264
Qy	181	CTTATCTCTGTAATAATAAAGGACTCAAAAGCGCTGGAAATATCTATCTCTTAAACTTG	240
Db	265	CTTATCTCTGTAATAATAAAGGACTCAAAAGCGCTGGAAATATCTATCTCTTAAACTTG	324
Qy	241	GCAGTTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300
Db	325	GCAGTTTCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	384
Qy	301	CCCATGTTAAATCTCATGGAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
Db	385	CCCATGTTAAATCTCATGGAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	444
Qy	361	AATTGCTCTGACTGTGCAAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	420
Db	445	AATTGCTCTGACTGTGCAAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	504
Qy	421	GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
Db	505	GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	564
Qy	481	CTGCGCACTTTCCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
Db	565	CTGCGCACTTTCCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	624
Qy	541	TGTGCATTTAGCAAGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
Db	625	TGTGCATTTAGCAAGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	684
Qy	601	ACTTTAAATATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
Db	685	ACTTTAAATATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	744
Qy	661	GTGCAATATGAATAAACAACACTAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAG	720
Db	745	GTGCAATATGAATAAACAACACTAAGGTTTCAAGGTTTCAAGGTTTCAAGGTTTCAAG	804
Qy	721	TTTGCCGTAATGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
Db	805	TTTGCCGTAATGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	864
Qy	781	TCCACTTTTCAAGAAACACTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
Db	865	TCCACTTTTCAAGAAACACTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	924
Qy	841	AGTGTTCATCATCAATAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
Db	925	AGTGTTCATCATCAATAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	984
Qy	901	GCGTTTCTGATGGGACATTTAGCAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Db	985	GCGTTTCTGATGGGACATTTAGCAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1044
Qy	961	ACCCCACTTCAACCCAGGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
Db	1045	ACCCCACTTCAACCCAGGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1104
Qy	1021	TCCACCGAAGTGTAA 1035	

Db	1105	TCCACCGAAGTGTA 1119
RESULT 3		
ABX95937		
ID	ABX95937	standard; cDNA; 1547 BP.
XX		
AC	ABX95937;	
XX		
DT	23-JUL-2003	(first entry)
XX		
DE	Human monocyte/dendritic cell receptor for chemokine (M/DC CR)	cDNA.
XX		
KW	Human; gene; ss; thymus expressed chemokine; TECK; chemokine; MIP-3alpha;	
KW	MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;	
KW	monocyte/dendritic cell receptor for chemokine; inflammatory condition;	
KW	abnormal physiology; abnormal proliferation; degeneration; atrophy;	
KW	antiinflammatory; antiasthmatic; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
XX		49. .1119
FT	CDS	/*tag= a
FT		/product= "Human M/DC CR"
FT		
XX		
PN	US2003018167-A1.	
XX		
PD	23-JAN-2003.	
XX		
PF	03-JAN-2002; 2002US-00039659.	
XX		
PR	05-JUL-1996; 96US-0021664P.	
PR	11-OCT-1996; 96US-0028329P.	
PR	04-JUN-1997; 97US-0048593P.	
PR	03-JUL-1997; 97US-00887977.	
XX		
PA	(SCHE) SCHERING CORP.	
XX		
PI	Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;	
XX		
DR	WPI; 2003-416900/39.	
DR	P-PSDB; ABU09081.	
XX		
PT	New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCR, useful	
PT	for treating conditions associated with abnormal physiology or	
PT	development, including inflammatory conditions (e.g. asthma), and	
PT	abnormal proliferation.	
PS	Claim 4; Page 8-9; 54pp; English.	
XX		
CC	The invention relates to nucleic acids encoding the chemokines TECK, MIP-	
CC	3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are	
CC	useful in isolating DNA clones encoding the chemokines, for generating	
CC	antibodies, and for predicting oligonucleotides for screening a library	
CC	to isolate species variants. A nucleic acid encoding a chemokine	
CC	polypeptide can be used to identify genes, mRNA and cDNA species which	
CC	encode related or homologous ligands, as well as DNA encoding homologous	
CC	proteins from different species. The chemokines and antibodies which bind	
CC	to the polypeptides are useful in the treatment of conditions associated	
CC	with abnormal physiology or development, including inflammatory	
CC	conditions such as asthma, abnormal proliferation, regeneration,	
CC	degeneration and atrophy. This sequence represents cDNA encoding the	
CC	human monocyte/dendritic cell receptor for chemokine (M/DC CR)	
CC	polypeptide	
XX		
SQ	Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;	
Query Match 100.0%; Score 1035; DB 10; Length 1547;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGCCCAATTACACGCTGGCAGACGATGAATATGATGCTCTCATAGAAGGTGAACCTG 60

Db 85 ATGCCCAATTAACAGCTGGCCAGAGGATGAATATGATGCTCTCATAGAGGTGAAGT 144
Qy 61 GAGAGGATGAGGAGGAGCAATGTGACAGATATGAGCCGAGGACCTCTCAGGCCAGGCTG 120
Db 145 GAGAGGATGAGGAGGAGCAATGTGACAGATATGAGCCGAGGACCTCTCAGGCCAGGCTG 204
Qy 121 GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 205 GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
Qy 181 CTTATCTCTGTAATAATATTAAGGACTCAACCGGCTGGAATAATCTATCTCTTAACCTTG 240
Db 265 CTTATCTCTGTAATAATATTAAGGACTCAACCGGCTGGAATAATCTATCTCTTAACCTTG 324
Qy 241 GCAGTTCTAACTTGTGTTCTTCTGCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 325 GCAGTTCTAACTTGTGTTCTTCTGCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384
Qy 301 CCATGCTGTAATAATCTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 385 CCATGCTGTAATAATCTCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
Qy 361 AATTGCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCTCA 420
Db 445 AATTGCTCTGACTGTGCAAGGTACTAGTGTGTTTGGCAAGGGCAACTTTTCTCTCA 504
Qy 421 GCCAGGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 505 GCCAGGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
Qy 481 CTGGCCACTTTGCTGTAATTCGTTGTTTATAAACCCTCAGATGGAAGCAGCAATCAAG 540
Db 565 CTGGCCACTTTGCTGTAATTCGTTGTTTATAAACCCTCAGATGGAAGCAGCAATCAAG 624
Qy 541 TGTGCTATTAGCAAGACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 625 TGTGCTATTAGCAAGACTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
Qy 601 ACTTTAAATAAGCAATTTCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 685 ACTTTAAATAAGCAATTTCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
Qy 661 GTGCAATGGAATAACACTTAAGGTTTCAAGGCGAGGATATAGCCTTTTCAAGCTTGT 720
Db 745 GTGCAATGGAATAACACTTAAGGTTTCAAGGCGAGGATATAGCCTTTTCAAGCTTGT 804
Qy 721 TTTGCCGTAATGCTAGTCTTCTTCTGATGCTGGCGCCCTACAAATATTGCAATTTTCCCTG 780
Db 805 TTTGCCGTAATGCTAGTCTTCTTCTGATGCTGGCGCCCTACAAATATTGCAATTTTCCCTG 864
Qy 781 TCCACTTTCAAGCAACTTCTCCCTGAGTGTGCTGCAAGAGAGCTACAAATCTGGAACAA 840
Db 865 TCCACTTTCAAGCAACTTCTCCCTGAGTGTGCTGCAAGAGAGCTACAAATCTGGAACAA 924
Qy 841 AGTGTTCACATCACTAACTCATGCGCCACCAACCCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 925 AGTGTTCACATCACTAACTCATGCGCCACCAACCCTGCTGCTGCTGCTGCTGCTGCTG 984
Qy 901 GCGTTTCTCATGAGCAATTTAGCAATACCTCTGCGGCTGTTTCAATCTGCGGTAGTAAC 960
Db 985 GCGTTTCTCATGAGCAATTTAGCAATACCTCTGCGGCTGTTTCAATCTGCGGTAGTAAC 1044
Qy 961 ACCCCACTTCAACCCGAGGAGCTGTGCAAGAGCAATCGAGGGGAAGAACTTGACCAT 1020
Db 1045 ACCCCACTTCAACCCGAGGAGCTGTGCAAGAGCAATCGAGGGGAAGAACTTGACCAT 1104
Qy 1021 TCCACCGAAGTGA 1035
Db 1105 TCCACCGAAGTGA 1119

ADQ67844
ID ADQ67844 standard; cDNA; 1547 BP.
XX
AC ADQ67844;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cDNA encoding chemokine receptor M/DCCR.
XX
KW Human; ss; gene; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;
KW Monocyte/dendritic cell receptor for chemokine; abnormal physiology;
KW development; inflammatory condition; asthma.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH CDS 49..1119
FT /*tag= a
FT /product= "Human M/DCCR"
XX
PN US2004137578-A1.
XX
PD 15-JUL-2004.
XX
PF 09-JAN-2004; 2004US-00754071.
XX
PR 05-JUL-1996; 96US-0021664P.
PR 11-OCT-1996; 96US-0028329P.
PR 04-JUN-1997; 97US-0048593P.
PR 03-JUL-1997; 97US-00887977.
PR 03-JAN-2002; 2002US-00039659.
XX
XX (WANG/) WANG W.
PA (GISH/) GISH K C.
PA (SCHA/) SCHALL T J.
PA (VICA/) VICARI A.
PA (ZLOT/) ZLOTNIK A.
XX
PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
XX
XX WPI; 2004-533376/51.
DR P-PSDB; ADQ67845.
XX
XX New substantially pure or isolated Thymus Expressed Chemokine (TECK).
XX useful for treating conditions associated with abnormal physiology or
XX development, including inflammatory conditions, e.g. asthma.
XX
XX Example 2; SEQ ID NO 11; 54pp; English.
XX
XX The invention relates to a substantially pure or isolated polypeptide
XX comprises the mature protein of human TECK (thymus expressed chemokine)
XX whose full length sequence appears as ADQ67837. Also included are an
XX isolated or recombinant nucleic acid encoding mature TECK, an expression
XX vector comprising the nucleic acid, a host cell comprising the expression
XX vector and a method for producing the polypeptide. Also disclosed are the
XX mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta
XX (and their encoding cDNAs), and the cDNAs and encoded proteins
XX corresponding to human chemokine receptors DCCR (dendritic cell receptor
XX for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for
XX chemokine). The polypeptide is useful for treating conditions associated
XX with abnormal physiology or development, including inflammatory
XX conditions, e.g. asthma. The present sequence encodes human chemokine
XX receptor M/DCCR.
XX
SQ Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 12; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCCCAATTAACAGCTGGCCAGAGGATGAATATGATGCTCTCATAGAGGTGAAGT 60
|||||

Db 328 ATGCCAATTRCACCTGGCACCAGAGGATGATGATGCTCTCATAGAGGTGAATCTG 387
Qy 61 GAGAGCGATGAGGACAGCAATGTGCAAGATATGACGCCAGGCACTCTCAGCCAGCTG 120
Db 388 GAGAGCGATGAGGACAGCAATGTGCAAGATATGACGCCAGGCACTCTCAGCCAGCTG 447
Qy 121 GTGCCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 448 GTGCCATCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507
Qy 181 CTTATCTCTGTAATAATATAAGGACTCAAAACGCGTGAATAATATCTATCTCTAACTTG 240
Db 508 CTTATCTCTGTAATAATATAAGGACTCAAAACGCGTGAATAATATCTATCTCTAACTTG 567
Qy 241 GCAATTTCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 568 GCAATTTCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
Qy 301 CCCATGCTGAATTTCTATTGGAATGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 628 CCCATGCTGAATTTCTATTGGAATGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
Qy 361 AATTGCTCTTGACTGTGCAAGGTACCTAGTGTGTTTTTTCACAGGCAACTTTTTCTCA 420
Db 688 AATTGCTCTTGACTGTGCAAGGTACCTAGTGTGTTTTTTCACAGGCAACTTTTTCTCA 747
Qy 421 GCCAGGAGGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 748 GCCAGGAGGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 807
Qy 481 CTGGCACTTTGCTGCAATTTGCTGTTTATTAACCTCAGATGGAAGACCAAGATACAAG 540
Db 808 CTGGCACTTTGCTGCAATTTGCTGTTTATTAACCTCAGATGGAAGACCAAGATACAAG 867
Qy 541 TGTGCATTTAGCAGAACTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 868 TGTGCATTTAGCAGAACTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
Qy 601 ACTTAAATAATGAACATTTCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 928 ACTTAAATAATGAACATTTCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
Qy 661 GTGCAATGAGAAACCACTAAGGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db 988 GTGCAATGAGAAACCACTAAGGTTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 1047
Qy 721 TTTGCGCTAATGCTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1048 TTTGCGCTAATGCTAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
Qy 781 TCCACTTTTCAAGAACACTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 1108 TCCACTTTTCAAGAACACTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
Qy 841 AGTGTTACATCACTAACTCATGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 1168 AGTGTTACATCACTAACTCATGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
Qy 901 GCGTTCTTGTAGGGACATTTAGCAATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1228 GCGTTCTTGTAGGGACATTTAGCAATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
Qy 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGACATGAGGGAAGAACCTTGACCAT 1020
Db 1288 ACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGACATGAGGGAAGAACCTTGACCAT 1347
Qy 1021 TCCACCGAAGGTAA 1035
Db 1348 TCCACCGAAGGTAA 1362

RESULT 7
ACH89585

ID XX ACH89585 standard; DNA; 1140 BP.
XX AC ACH89585;
XX DT 29-JUL-2004 (first entry)
XX DE Human genome derived single exon probe #22780.
XX KW Human; probe; ss; gene expression; single exon probe; microarray;
XX OS alternative splicing event; genomic alteration.
XX OS Homo sapiens.
XX PN US2003194704-A1.
XX PD 16-OCT-2003.
XX PF 03-APR-2002; 2002US-00029386.
XX PR 03-APR-2002; 2002US-00029386.
XX PA (PENN/) PENN S G.
XX PA (RANK/) RANK D R.
XX PA (HANZ/) HANZEL D K.
XX PI Penn SG, Rank DR, Hanzel DK;
XX WI MPI; 2004-119264/12.
XX PT New human genome-derived single exon nucleic acid probes useful for human
XX PT gene expression analysis, for identifying or characterizing alternative
XX PT splicing events, for assessing genomic alterations or as tools for
XX PT surveying tissues.
XX PT Claim 1; SEQ ID NO 22780; 80pp; English.
XX CC The invention relates to a nucleic acid probe for measuring human gene
XX CC expression, comprising any of the 27,400 fully defined nucleotide
XX CC sequences in the specification, or their complements or fragments, and
XX CC encoding at least 8 amino acids of any of the 688 amino acid sequences
XX CC fully defined in the specification. The probe is a single exon probe that
XX CC hybridises under high stringency conditions to a nucleic acid molecule
XX CC expressed in human cells or tissues. Also included are a spatially-
XX CC addressable set of single exon nucleic acid probes for measuring human
XX CC gene expression (comprising a plurality of single exon nucleic acid
XX CC probes cited above, where each of the plurality of probes is separately
XX CC and addressably isolatable or amplifiable from the plurality), a single
XX CC exon microarray for measuring human gene expression, a method of
XX CC measuring human gene expression, a vector comprising the single exon
XX CC probe cited above, an ORF-encoded peptide comprising at least 8
XX CC contiguous amino acids of any of the above-mentioned amino acid
XX CC sequences (optionally with conservative amino acid substitutions), an
XX CC isolated antibody that binds specifically to a peptide cited above,
XX CC methods of selling and/or licensing single exon probes or microarrays to
XX CC a customer desiring to measure gene expression, a method of providing
XX CC human gene expression data by subscription, and a computer-readable
XX CC storage medium which contains a database having a plurality of records
XX CC (each record including data on the expression of a single exon probe
XX CC cited above. The probe, methods and apparatus are useful in gene
XX CC expression analysis. The probes may be used as tools for surveying
XX CC tissues to detect the presence of expressed messages that contain their
XX CC specific exon, or in constructing genome-derived single exon microarrays.
XX CC In addition, the probes are used in identifying and characterising
XX CC alternative splicing events, in detecting and characterising gross
XX CC alterations in the genomic locus that includes their exon, in assessing
XX CC smaller genomic alterations, in priming the synthesis of nucleic acids,
XX CC or in expressing the ORF-encoded peptide. The present sequence is a human
XX CC single exon probe of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from USPTO at
XX CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX SQ Sequence 1140 BP; 294 A; 275 C; 241 G; 330 T; 0 U; 0 Other;

cardiovascular disorder; endothelial disorder; angiogenic disorder;
myocardial infarction; cardiac hypertrophy; trauma; cancer;
age-related macular degeneration; angiogenesis;
endothelial cell apoptosis; smooth muscle cell growth;
endothelial cell tube formation.

Homo sapiens.

US2003105011-A1.
05-JUN-2003.

16-AUG-2002; 2002US-00223084.

15-SEP-2000; 2000US-0232887P.
20-JUN-2001; 2001WO-US019692.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2003-810831/76.
P-PSDB; ADD10305.

New isolated nucleic acid encoding a secreted and transmembrane polypeptide for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular degeneration.

Claim 2; SEQ ID NO 15; 493pp; English.

The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterized by the presence of an elevated level of pG-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial cell growth in a mammal. PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis. PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to stimulate or inhibit smooth muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.

Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 99.7%; Score 1031.8; DB 10; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGCCCAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 60
29 ATGCCCAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAGGTGAACCTG 88
61 GAGAGCGATGAGGAGGAGGATGACAAAGTATGACGCCCGCCAGGCACTCTCAGCCGAGCTG 120
89 GAGAGCGATGAGGAGGAGGATGACAAAGTATGACGCCCGCCAGGCACTCTCAGCCGAGCTG 148
121 GTGCCATCACTCTCTCTGCTGCTTTGATGTCGGTGTCTGGACAATCTCTGCTGTTGTG 180
149 GTGCCATCACTCTCTCTGCTGCTTTGATGTCGGTGTCTGGACAATCTCTGCTGTTGTG 208
181 CTTATCTCTGTAATAATATAAGGACTCAACCGCTGGAAATATCTATCTCTTAACCTTG 240
209 CTTATCTCTGTAATAATATAAGGACTCAACCGCTGGAAATATCTATCTCTTAACCTTG 268

Qy 241 GCAGTTTCTAACTTGTGTTTCTTCTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGCAT 300
Db 269 GCAGTTTCTAACTTGTGTTTCTTCTTACCTCGCCCTTCTGGGCTCATGCTGGGGCGCAT 328
Qy 301 CCCATGTGTAATAATCTCATTTGGACTGTACTTCTGCTGGCCCTGTACAGTGAGACATTTTTC 360
Db 329 CCCATGTGTAATAATCTCATTTGGACTGTACTTCTGCTGGCCCTGTACAGTGAGACATTTTTC 388
Qy 361 AATTGCTCTCTGACTGTGCAAGGTAAGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420
Db 389 AATTGCTCTCTGACTGTGCAAGGTAAGTACTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 448
Qy 421 GCCAGGAGGAGGCTGCTGCTGTCGATCATTTACAAGTGTCTGGCATGGGTAAAGCCATT 480
Db 449 GCCAGGAGGAGGCTGCTGCTGTCGATCATTTACAAGTGTCTGGCATGGGTAAAGCCATT 508
Qy 481 CTGSCCACTTTGCTGCTGAATTCGTGTTTATAAACTCAGATGGAAGACCAAGAAATACAAG 540
Db 509 CTGSCCACTTTGCTGCTGAATTCGTGTTTATAAACTCAGATGGAAGACCAAGAAATACAAG 568
Qy 541 TGTGCATTTAGCAGAACTCCCTTCTGCTGCTGATGAGACATTTCTGGAAGCAATTTCTG 600
Db 569 TGTGCATTTAGCAGAACTCCCTTCTGCTGCTGATGAGACATTTCTGGAAGCAATTTCTG 628
Qy 601 ACTTTAAATAATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 629 ACTTTAAATAATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
Qy 661 GTGCAATGAGAAACACATTAAGTTTCAGGAGGAGGAGGATATAGCCTTTTCAAGCTGTT 720
Db 689 GTGCAATGAGAAACACATTAAGTTTCAGGAGGAGGAGGATATAGCCTTTTCAAGCTGTT 748
Qy 721 TTTGCCCTAATGAGTGTGCTTCTTCTGATGTGGCGCCCTACAAATATTTGCAATTTTCTG 780
Db 749 TTTGCCCTAATGAGTGTGCTTCTTCTGATGTGGCGCCCTACAAATATTTGCAATTTTCTG 808
Qy 781 TCACATTTTCAAGAAACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 809 TCACATTTTCAAGAAACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 868
Qy 841 AGTTTTCACATCACTAACTATGCAATATTTAGCAATATTTAGCAATATTTAGCAATATTT 900
Db 869 AGTTTTCACATCACTAACTATGCAATATTTAGCAATATTTAGCAATATTTAGCAATATTT 928
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Db 929 GCGTTTCTGATGGGACATTTAGCAATATTTAGCAATATTTAGCAATATTTAGCAATATTT 988
Qy 961 ACCCACTTCAACCCAGGGGCGAGTCTGCAAGGCAATCGAGGAGAAACCTTGACCAT 1020
Db 989 ACCCACTTCAACCCAGGGGCGAGTCTGCAAGGCAATCGAGGAGAAACCTTGACCAT 1048
Qy 1021 TCCACCGAAGTGTA 1035
Db 1049 TCCACCGAAGTGTA 1063

RESULT 11
ADD11264
ID ADD11264 standard; cDNA; 1475 BP.
XX
AC ADD11264;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide cDNA #8.
XX
KW ss; gene; human; secreted protein; transmembrane protein;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; angiogenesis;
KW endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.

PD XX 05-JUN-2003.
 PF XX 16-AUG-2002; 2002US-00223088.
 PR XX 15-SEP-2000; 2000US-0232887P.
 PR XX 20-JUN-2001; 2001WO-US019692.
 PR XX 09-JUL-2001; 2001WO-US021735.
 PR XX 20-FEB-2002; 2002US-00081056.
 XX XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski RJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JP;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2003-829354/77.
 DR P-PSDB; ADD37058.
 XX
 XX New isolated nucleic acids encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX
 XX Claim 2; SEQ ID NO 15; 492pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents a cDNA encoding a
 CC PRO polypeptide of the invention.
 XX
 SQ Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 99.7%; Score 1031.8; DB 10; Length 1475;
 Best Local Similarity 99.8%; Pred. NO. 0;
 Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCAAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAAGGTGAACCTG 60
 DB 29 ATGGCCAAATTACAGCTGGCCACGAGGATGAATATGATGTCCTCATAGAAGGTGAACCTG 88
 QY 61 GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACTCTCAGCCACGCTG 120
 DB 89 GAGAGCGATGAGGAGAGCAATGTGACAAGTATGACGCCAGGCACTCTCAGCCACGCTG 148
 QY 121 GTGCCATCAGCTCTGCTCTGCTGTGTGTGTGATCGGTGTCTGGACAATCTCTCTGTTGTG 180
 DB 149 GTGCCATCAGCTCTGCTCTGCTGTGTGTGTGATCGGTGTCTGGACAATCTCTCTGTTGTG 208
 QY 181 CTTATCTCTGGTAAATATAAAGGACTCAACCGGTGGAAATATCTATCTCTTAAACCTTG 240
 DB 209 CTTATCTCTGGTAAATATAAAGGACTCAACCGGTGGAAATATCTATCTCTTAAACCTTG 268
 QY 241 GCAGTTTCTACTTGTGTGTCTTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 269 GCAGTTTCTACTTGTGTGTGTCTTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 328
 QY 301 CCCATGTGTAATATCTCATTTGGGACTGTACTTCTGGGCTGTGACAGTGAGACATTTTTC 360
 DB 329 CCCATGTGTAATATCTCATTTGGGACTGTACTTCTGGGCTGTGACAGTGAGACATTTTTC 388
 QY 361 AATTGCCCTTCTGATGTGCAAGGTA CTTAGTGTGTTTGTGCAAGGGCAACTTTTCTCA 420

DB 389 AATTGCCCTTCTGATGTGCAAGGTACTAGTGTGTTTTTGCACAGGGCAACTTTTCTCA 448
 QY 421 GCCAGGAGGAGGTGCTCCTGTGGCATCATTAACAAGTGTCTGTGGCATGGTAAACAGCCATT 480
 DB 449 GCCAGGAGGAGGTGCTCCTGTGGCATCATTAACAAGTGTCTGTGGCATGGTAAACAGCCATT 508
 QY 481 CTGGCCACTTTTGCCTGAATTCGTGTTTATAAACCCTCAGATGGAAGACGACGAGAAATACAAG 540
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 QY 541 TGTGCATTTAGCAGAACTCCCTTCTGCCAGCTGATGAGACATTCCTGGAAGCATTTTCTG 600
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 QY 601 ACTTTAAAAATGAACATTTTCGTTCTTGTCTCTCCCTTATTTATTTTACATTTCTCTAT 660
 DB 629 ACTTTAAAAATGAACATTTTCGTTCTTGTCTCTCCCTTATTTATTTTACATTTCTCTAT 688
 QY 661 GTGCAATGAGAAAACACTAAGGTTCAGGAGGACGAGGTATAGCCTTTTCAAGCTTGT 720
 DB 689 GTGCAATGAGAAAACACTAAGGTTTCAAGGTTCAAGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 748
 QY 721 TTTCCGCTAATGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGTCATTTTCTG 780
 DB 749 TTTGCCATTAATGGTAGTCTTCTCTGATGTGGGCGCCCTACAATATTGTCATTTTCTG 808
 QY 781 TCCACTTTTCAAGAAACACTTCTCCTGTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 840
 DB 809 TCCACTTTTCAAGAAACACTTCTCCTGTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 868
 QY 841 AGTGTTCACATCACTAACTCATGCCACCACTGCTGTCATCAACCCCTCTCTCTGAT 900
 DB 869 AGTGTTCACATCACTAACTCATGCCACCACTGCTGTCATCAACCCCTCTCTCTGAT 928
 QY 901 GCGTTTCTTGAATGGAGCATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
 DB 929 GCGTTTCTTGAATGGAGCATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 988
 QY 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCACATCGAGGGAAGAACCTTGACCAT 1020
 DB 989 ACCCCACTTCAACCCAGGGGCGAGTCTGCAACAGGCACATCGAGGGAAGAACCTTGACCAT 1048
 QY 1021 TCCACCGAAGTGTAA 1035
 DB 1049 TCCACCGAAGTGTAA 1063

RESULT 13
 ADE41265
 ID ADE41265 standard; cDNA; 1475 BP.
 XX
 AC ADE41265;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human secreted/transmembrane PRO polypeptide cDNA #8.
 XX
 KW ss: gene; human; secreted protein; transmembrane protein;
 KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
 KW myocardial infarction; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; angiogenesis;
 KW endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 PN US2003100497-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 16-AUG-2002; 2002US-00223085.
 XX
 PR 20-JUN-2001; 2001WO-US019692.
 PR

PI Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W;
XX
DR WPI; 2004-042166/04.
DR P-ESDB; ADH43449.

New PRO polypeptides and nucleic acids encoding the polypeptides, useful for treating myocardial infarction, cardiac hypertrophy, trauma, cancer, or age-related macular degeneration.

PS Claim 2; SEQ ID NO 15; 492pp; English.

The invention relates to human PRO polypeptides and the PRO polynucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial cell growth, stimulating endothelial cell growth, inducing cardiac hypertrophy, cell apoptosis or cell tube formation and stimulating angiogenesis or smooth muscle cell growth by administering polypeptides of the invention. The PRO polypeptides and polynucleotides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO polynucleotides are useful as hybridisation probes in chromosome and gene mapping and in generating antisense RNA and DNA, and for chromosome identification and tissue typing. The PRO polypeptides and polynucleotides are also useful in gene therapy and as molecular weight markers for protein electrophoresis purposes. This sequence represents a human PRO polynucleotide of the invention.

Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

Query Match 99.7%: Score 1031.8: DB 12: Length 1475:

Query Match	99.7%	Score IV31:8
Best Local Similarity	99.8%	Pred. No. 0;

2000 Local similarity 33.60% 12000
 Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGCCCAATTACAGCTGGCACGAGAGTGAATATGATGTCCTCATGAAGGTTGAAC	60
Db	29	ATGGCCAAATTACAGCTGGCACGAGAGGATGAATATGATGTCCTCATGAAGGTTGAAC	88
Qy	61	GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCACAGGCAC	120
Db	89	GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCACAGGCAC	148
Qy	121	GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTGGACAATCTCCTCGTTGTG	180
Db	149	GTGCCATCACTCTGCTCTGCTGTGTTGTGATCGGTGTCTGGACAATCTCCTCGTTGTG	208
Qy	181	CTTATCTGTGTAATAATAAAGGACTCAACCGCTGGAAATATCTATCTTTCTAAACTG	240
Db	209	CTTATCTGTGTAATAATAAAGGACTCAACCGCTGGAAATATCTATCTTTCTAAACTG	268
Qy	241	GCAGTTTCTAACTGTGTTCTTGCTGTACCCCTGCTGCGGCTCATGCTGGGGCGAT	300
Db	269	GCAGTTTCTAACTGTGTTCTTGCTGTACCCCTGCTGCGGCTCATGCTGGGGCGAT	328
Qy	301	CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGTGAGACAT	360
Db	329	CCCATGTGTAAATTTCTCATTTGGACTGTACTTCTGTGGGCCCTGTACAGTGAGACAT	388
Qy	361	AAATTGCCCTTCTGACTGTGCAAGGTACCTAGTGTGTTTTTGTGCAAGGGCAACTTTT	420
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PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 02-JUN-1999; 99WO-US012252.
PR 14-JUN-1999; 99US-00333228.
PR 14-JUN-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 15-OCT-1999; 99US-00403154.
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PR 18-OCT-1999; 99US-00403297.
PR 10-NOV-1999; 99US-00423741.
PR 12-NOV-1999; 99US-00423843.
PR 12-NOV-1999; 99US-00423844.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
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PR 01-DEC-1999; 99WO-US028634.
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PR 30-DEC-1999; 99WO-US031243.
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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
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PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
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PR 10-MAR-2000; 2000WO-US006319.
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PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US015264.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
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PR 24-AUG-2000; 2000WO-US023328.
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PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 10-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 05-APR-2001; 2001US-00828366.
PR 25-MAY-2001; 2001US-00866028.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 04-SEP-2001; 2001US-00946374.
PR 07-SEP-2001; 2001US-00948901.
PR 15-NOV-2001; 2001US-00002796.
PR 30-NOV-2001; 2001US-00001054.
PR 06-DEC-2001; 2001US-00006867.
PR 19-DEC-2001; 2001US-00028072.
PR 15-JAN-2002; 2002US-00052586.
PR 17-JAN-2002; 2002US-00053107.
PR 18-JAN-2002; 2002US-00052594.
PR 08-FEB-2002; 2002US-00072068.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2004-225727/21.
DR P-PSDB; ADK82794.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 2; SEQ ID NO 15; 494pp; English.
XX
XX The invention relates to human PRO polypeptides and the PRO
CC polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
CC polynucleotide of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
SQ
Query Match 99.7%; Score 1031.8; DB 12; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGCCCAATTACACGCTGGCACAGAGGATGAATATGATGCTCTCTATAGAAGTGAACTG 60
Db 29 ATGCCCAATTACACGCTGGCACAGAGGATGAATATGATGCTCTCTATAGAAGTGAACTG 88
Qy 61 GAGAGCGATGAGGACAGACGCAATGTGCAAGTATGACGCCGAGCACTCTCAGCCAGCTG 120
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Db 149 GTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCCTGACAAATCTCTCGTTGTG 208
Qy 181 CTTATCTCTGGTAAATATATAAGGACTCAAACGGCTGGAATAATCTATCTTCTTAACCTG 240
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Db      389 AATTGCCCTTCTGACTGTGCAAGGTAGCTAGTGTGTTTTTGACAAGGGCAACTTTTCTCA 448
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Qy      481 CTGGCCACTTTGCTGCTGAATTCGTGGTTTATAAACCCTCAGATGGAGACCAAGATACAAG 540
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Qy      541 TGTGCATTTAGCAGAACTCCCTTCTGCTGAGCTCATGAGACATTTCTGGAAGCATTTTCTG 600
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Qy      601 ACTTTAAAAATGAACATTTGGTTCTTGTCTCTCCCTCTATTTATTTTACATTTTCTCTAT 660
Db      629 ACTTTAAAAATGAACATTTGGTTCTTGTCTCTCCCTCTATTTATTTTACATTTTCTCTAT 688
Qy      661 GTGCAATAGAAATAACACTAAGTTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 720
Db      689 GTGCAATAGAAATAACACTAAGTTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGT 748
Qy      721 TTTGCGGTAAATGGTAGTCTTCTCTGATGTGGGCGCTTACATATTTGCAATTTTCTCTG 780
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Qy      841 AGTGTTCACATCACTAACTCATGCGCACCACTGCTGCTGCAATCAACCTCTCTCTGTAT 900
Db      869 AGTGTTCACATCACTAACTCATGCGCACCACTGCTGCTGCAATCAACCTCTCTCTGTAT 928
Qy      901 GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 960
Db      929 GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCGCTGTTTCCATCTGCGTAGTAAC 988
Qy      961 ACCCACTTCAACCCAGGGGGAGTCTGCGACAGGCACATCGAGGGAGAACCTTGACCAT 1020
Db      989 ACCCACTTCAACCCAGGGGGAGTCTGCGACAGGCACATCGAGGGAGAACCTTGACCAT 1048
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Db      1049 TCCACCGAAGTGTA 1063
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Search completed: June 18, 2005, 07:10:37
Job time : 646.224 Secs

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CC capable of being expressed on brain glial cells and is known in the mouse
CC as L-CCR or in humans as CCR-2. The chemokine receptor expressed in a
CC cultured cell comprising the cell transfected with a nucleic acid and a
CC HEK cell, is useful in identifying a candidate drug compound for treating
CC inflammatory or degenerative brain disease, e.g. ischaemia, Alzheimer's
CC disease or multiple sclerosis. The agonist or antagonist is useful in the
CC preparation of the pharmaceutical composition useful in treating
CC neurodegenerative and neuroinflammatory diseases such as allergic
CC encephalitis and chronic obstructive pulmonary disease and obstructive
CC airway diseases such as asthma. This sequence represents human CCR-2
CC cDNA, also known as CCR2
XX
SQ Sequence 1035 BP; 255 A; 255 C; 228 G; 297 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 6; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCCAAATACAGCTGGGACACAGAGGATGAATATGATGTCCTCATAGAGGTGAAGCTG 60
DB 1 ATGGCCAAATACAGCTGGGACACAGAGGATGAATATGATGTCCTCATAGAGGTGAAGCTG 60
QY 61 GAGAGCGATGAGGACAGAGCAATGTGACAGATGATGACGCGCCAGGCACTCTCAGCCAGCTG 120
DB 61 GAGAGCGATGAGGACAGAGCAATGTGACAGATGATGACGCGCCAGGCACTCTCAGCCAGCTG 120
QY 121 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GTGCCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CTATCTCTGTAATATATAGAGGACTCAAGCGCTGGAAATATCTATCTCTTAAACTTG 240
DB 181 CTATCTCTGTAATATATAGAGGACTCAAGCGCTGGAAATATCTATCTCTTAAACTTG 240
QY 241 GCAGTTCTTAACTTGTGTTCTTGTGTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCAGTTCTTAACTTGTGTTCTTGTGTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 CCCATGTGTAATATCTCAATGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 CCCATGTGTAATATCTCAATGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 AATGCTCTTCTGACTGCTCAAGAGTACCTAGTGTGTTGTTGCAAGGGCAACTTTTCTCA 420
DB 361 AATGCTCTTCTGACTGCTCAAGAGTACCTAGTGTGTTGTTGCAAGGGCAACTTTTCTCA 420
QY 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTGGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 CTGGCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TGTGCTTTAGCGAAGCTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TGTGCTTTAGCGAAGCTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 ACTTTAAATATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 ACTTTAAATATGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 GTGCAATATGAGAAACAACTAAGTTCTAGGAGGAGGAGGATAGGCTTTTCAAGCTGTT 720
DB 661 GTGCAATATGAGAAACAACTAAGTTCTAGGAGGAGGAGGATAGGCTTTTCAAGCTGTT 720
QY 721 TTTGCGGTAATGAGTGTCTCTTCTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 TTTGCGGTAATGAGTGTCTCTTCTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TCCACTTTTCAAGAACACATTTCTCCCTGAGTGTGCTGCAAGAGCAGCTTACATCTCGACAAA 840
DB 781 TCCACTTTTCAAGAACACATTTCTCCCTGAGTGTGCTGCAAGAGCAGCTTACATCTCGACAAA 840

QY 841 AGTGTTCACATCACTAAATCTATCGCCACACCCACTGTGTGATCAACCCCTCTCTGTAT 900
DB 841 AGTGTTCACATCACTAAATCTATCGCCACACCCACTGTGTGATCAACCCCTCTCTGTAT 900
QY 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC 960
DB 901 GCGTTTCTGATGGGACATTTAGCAATACCTCTGCGGCTGTTTCCATCTGCGTAGTAAC 960
QY 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGCACTCTGCAAGGCAAGAACCTTGACCAT 1020
DB 961 ACCCCACTTCAACCCAGGGGCGAGTCTGCAAGGCACTCTGCAAGGCAAGAACCTTGACCAT 1020
QY 1021 TCCACCGAAGTGTAA 1035
DB 1021 TCCACCGAAGTGTAA 1035
RESULT 2
ID AAV15419 standard; cDNA; 1547 BP.
XX AAV15419
AC AAV15419;
XX 11-JUN-1998 (first entry)
XX Human macrophage/dendritic cell chemokine receptor encoding cDNA.
XX Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor;
XX dendritic cell; macrophage; inflammation; asthma; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 49..1119
XX /*tag= a
XX /product= "M/DC CR"
XX /note= "macrophage/dendritic cell chemokine receptor"
XX W09801557-A2.
XX 15-JAN-1998.
XX 02-JUL-1997; 97WO-US010819.
XX 05-JUL-1996; 96US-00675814.
XX 11-OCT-1996; 96US-0028229P.
XX 04-JUN-1997; 97US-0048593P.
XX (SCHE) SCHERING CORP.
XX Gish KC, Schall TJ, Vicari A, Zlotnik A, Wang W;
XX WPI, 1998-101054/09.
XX P-PSDB; AAW48087.
XX Novel chemokines, e.g. thymus expressed chemokine - used for treating
XX inflammatory conditions including asthma.
XX Claim 5; Page 95-97; 202pp; English.
XX The present sequence encodes human macrophage/dendritic cell chemokine
XX receptor. Antibodies which bind to the protein can be used in detecting
XX or diagnosing various immunological conditions related to expression of
XX the protein. The nucleic acid can be used for screening and isolating DNA
XX clones for the chemokines, especially from other species. The chemokine
XX can be used in the treatment of conditions associated with abnormal
XX physiology or development, including inflammatory conditions such as
XX asthma
SQ Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 2; Length 1547;

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Best Local Similarity 100.0%; Pred. No. 0;		Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGCCAAATTACACGCTGACAGGAGTGAATATGATGCTCTCATAGAGTGAACCTG	60
DB	85	ATGGCCAAATTACACGCTGACAGGAGTGAATATGATGCTCTCATAGAGTGAACCTG	144
QY	61	GAGAGCGATGAGCGAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCAGCTG	120
DB	145	GAGAGCGATGAGCGAGAGCAATGTGCAAGTATGACGCCAGGCACTCTCAGCCAGCTG	204
QY	121	GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180
DB	205	GTGCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	264
QY	181	CTTATCTCTGTAATAATATAAGGACTCAAAACGCTGGAATAATCTATCTCTTAACTG	240
DB	265	CTTATCTCTGTAATAATATAAGGACTCAAAACGCTGGAATAATCTATCTCTTAACTG	324
QY	241	GCAGTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300
DB	325	GCAGTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	384
QY	301	CCCATGTGTAAATCTCAATGGAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
DB	385	CCCATGTGTAAATCTCAATGGAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	444
QY	361	AAATGCTCTCTGACTGTGCAAGGTAACCTAGTGTGTTTGGCAAGGCAACTTTTCTCA	420
DB	445	AAATGCTCTCTGACTGTGCAAGGTAACCTAGTGTGTTTGGCAAGGCAACTTTTCTCA	504
QY	421	GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
DB	505	GCCAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	564
QY	481	CTGGCCACTTTGCTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
DB	565	CTGGCCACTTTGCTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	624
QY	541	TGTGCTATTAGCAGAACTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
DB	625	TGTGCTATTAGCAGAACTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	684
QY	601	ACTTTAAATGAAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
DB	685	ACTTTAAATGAAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	744
QY	661	GTGCAATGAGAAACACTTAAGGTTGAGGAGGAGGATAGGCTTTTCAAGCTTGT	720
DB	745	GTGCAATGAGAAACACTTAAGGTTGAGGAGGAGGATAGGCTTTTCAAGCTTGT	804
QY	721	TTTGCCGTAATGTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
DB	805	TTTGCCGTAATGTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	864
QY	781	TCCACTTTCAAGAAACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
DB	865	TCCACTTTCAAGAAACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	924
QY	841	AGTGTTCACATCACTAACTCATGCGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
DB	925	AGTGTTCACATCACTAACTCATGCGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	984
QY	901	GGGTTCCTGATGAGCAATTTAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
DB	985	GGGTTCCTGATGAGCAATTTAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1044
QY	961	ACCCCACTTCAACCCAGGGGGAGTCTGCAAGGCACTCGAGGGAAGAACTGACCAT	1020
DB	1045	ACCCCACTTCAACCCAGGGGGAGTCTGCAAGGCACTCGAGGGAAGAACTGACCAT	1104
QY	1021	TCACCGAAGTGTA 1035	

Db	1105	TCCACCGAAGTGTA 1119
RESULT 3		
ABX95937		
ID	ABX95937	standard; cDNA, 1547 BP.
XX		
AC	ABX95937;	
XX		
DT	23-JUL-2003	(first entry)
XX		
DE	Human monocyte/dendritic cell receptor for chemokine (M/DC CR)	cDNA.
XX		
KW	Human; gene; ss; thymus expressed chemokine; TECK; chemokine; MIP-3alpha;	
KW	MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;	
KW	monocyte/dendritic cell receptor for chemokine; inflammatory condition;	
KW	abnormal physiology; abnormal proliferation; degeneration; atrophy;	
KW	antiinflammatory; antiasthmatic; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
CDS	49..1119	
FT	/*tag= a	
FT	/product= "Human M/DC CR"	
XX		
FN	US2003018167-A1.	
XX		
PD	23-JAN-2003.	
XX		
PF	03-JAN-2002; 2002US-00039659.	
XX		
PR	05-JUL-1996; 96US-0021664P.	
PR	11-OCT-1996; 96US-0028329P.	
PR	04-JUN-1997; 97US-0048593P.	
PR	03-JUL-1997; 97US-00887977.	
XX		
PA	(SCHE) SCHERING CORP.	
XX		
PI	Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;	
XX		
DR	WPI; 2003-416900/39.	
DR	P-PSDB; ABU09081.	
XX		
PT	New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful	
PT	for treating conditions associated with abnormal physiology or	
PT	development, including inflammatory conditions (e.g. asthma), and	
PT	abnormal proliferation.	
XX		
PS	Claim 4; Page 8-9; 54pp; English.	
XX		
CC	The invention relates to nucleic acids encoding the chemokines TECK, MIP-	
CC	3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are	
CC	useful in isolating DNA clones encoding the chemokines, for generating	
CC	antibodies, and for predicting oligonucleotides for screening a library	
CC	to isolate species variants. A nucleic acid encoding a chemokine	
CC	polypeptide can be used to identify genes, mRNA and cDNA species which	
CC	encode related or homologous ligands, as well as DNA encoding homologous	
CC	proteins from different species. The chemokines and antibodies which bind	
CC	to the polypeptides are useful in the treatment of conditions associated	
CC	with abnormal physiology or development, including inflammatory	
CC	conditions such as asthma, abnormal proliferation, regeneration,	
CC	degeneration and atrophy. This sequence represents cDNA encoding the	
CC	human monocyte/dendritic cell receptor for chemokine (M/DC CR)	
CC	polypeptide	
XX		
SQ	Sequence 1547 BP; 434 A; 357 C; 329 G; 427 T; 0 U; 0 Other;	
Query Match 100.0%; Score 1035; DB 10; Length 1547;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGGCAATTACAGCTGGCACGAGAGATGAATATGATGCTCTCATAGAGTGAACCTG 60

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